

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 11, 2002, 02:43:44 : Search time 3214 Seconds
(without alignments)
11277.150 Million cell updates/sec

Title: US-09-530-233-1
Perfect score: 1732
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: gb.pat:*
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33: em.htg.inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1732	100.0	1732	6	AX286634	AX286634 Sequence
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6	1653.6	95.5	1736	9	AB010575	AB010575 Homo sapi
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11	1508.2	87.1	1711	6	A82595	A82595 Sequence 3
12	1508.2	87.1	1711	6	A82768	A82768 Sequence 1
13	1096.4	63.3	1602	6	A87685	A87685 Sequence 5
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ALIGNMENTS

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DEFINITION Sequence 1 from Patent WO9921981.
ACCESSION A97008
VERSION A97008.1 GI:6780449
KEYWORDS
SOURCE
ORGANISM
unidentified.
unclassified.
REFERENCE 1 (bases 1 to 1732)
Babinski, K. and Seguela, P.
TITLE DNA ENCODING A HUMAN PROTON-GATED ION CHANNEL AND USES THEREOF
JOURNAL Patent: WO 9921981-A 1 06-MAY-1999;
UNIV MCGILL (CA); BABINSKI KAZIMIERZ (CA)
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ORIGIN

Query Match 100.0%; Score 1732; DB 6; Length 1732;
Best Local Similarity 100.0%; Pred. No. 2,1e-288;
Matches 1732; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
LOCUS AX286634 1732 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 3 from Patent W00181570.
ACCESSION AX286634
VERSION AX286634.1 GI:17048709
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (sites)
 AUTHORS Seguela, P. and Babin, K.
 TITLE Heteromultimeric ion channel receptor and uses thereof
 JOURNAL Patent: WO 0181570-A 3 01-NOV-2001;
 MCGILL UNIVERSITY (CA)
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 Best Local Similarity 100.0%; Pred. No. 2.1e-288;
 Matches 1732; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 complete cds.
 ACCESSION AF057711
 VERSION AF057711.1 GI:3702835
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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REFERENCE      1 (bases 1 to 1732)
AUTHORS        Babinski, K., Le, K.-T. and Seguela, P.
TITLE          Cloning, functional properties and distribution of a
                non-desensitizing proton-gated channel from human brain
JOURNAL        unpublished
REFERENCE      2 (bases 1 to 1732)
AUTHORS        Babinski, K., Le, K.-T. and Seguela, P.
TITLE          Direct Submersion
JOURNAL        Submitted (06-APR-1998) Neurology & Neurosurgery, Montreal
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                Canada

FEATURES
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BASE COUNT     326 a      601 c      484 g      321 t
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Query Match      100.0%; Score 1732; DB 9; Length 1732;
Best Local Similarity 100.0%; Pred. No. 2,1e-286;
Matches 1732: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION	Homo sapiens proton-gated cation channel ASIC3 mRNA, complete cds.		
ACCESSION	AF095897		
VERSION	AF095897.1		
KEYWORDS	GI:3747100		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Mammalia: Eutheria: Chordata: Craniata: Vertebrata: Euteleostomi;		
AUTHORS	1 (bases 1 to 1746)		
TITLE	de Welle, J.R., Bassilana, F., Lazdunski, M. and Waldmann, R.		
JOURNAL	Identification, functional expression and chromosomal localisation		
MEDLINE	of a sustained human proton-gated cation channel		
REFERENCE	FEBs Lett. 433 (3), 257-260 (1998)		
AUTHORS	2 (bases 1 to 1746)		
JOURNAL	de Welle, J.R., Bassilana, F., Lazdunski, M. and Waldmann, R.		
TITLE	Direct Submission		
FEATURES	Submitted (26-SEP-1998) IMPC, CNRS, University of Nice/Sophia		
source	Antipolis, 660 Route des Lucioles, 06560 Valbonne 06560, France		
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	LIDPRFKQRCGPENPTTITFRMRKCTTFNSGADGAEILITTRGMGGLDILMDVQ		
	EEYIYVWRNDNEETFEVGIKQIHSDDEPILIDLGVSQYGFVSQDQQLSFLE		
	PPWDCSSASLNPVNEPEPDPGLGSPSPSPPTLMGCRACETRYARCGGRMYV		
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OY	123	GCACGAGAGCTGAGCTGCGCGCGGGGAGATGTGTGGCAGCGCGCGGTGTCTGTCAGTGTGGC	182
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ARI68531 1736 bp DNA linear PAT 17-DEC-2001
LOCUS DEFINITION Sequence 13 from patent US 6287859.
ACCESSION ARI68531
VERSION ARI68531.1 GI:17904498
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1736)
AUTHORS DeMulle,J.R., Bassilana,F., Lazdunski,M. and Rahner,W.
TITLE Identification, functional expression and chromosomal localization of
a sustained human proton-gated cation channel
JOURNAL Patent: US 6287859-A 13 11-SEP-2001;
FEATURES
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location/Qualifiers
BASE COUNT 335 a 596 c 486 g 319 t
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RESULT 6
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 AB010575
 AB010575.1 GI:3097313
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS Ishibashi, K.
 TITLE Direct Submission
 JOURNAL Submitted (20-JAN-1998) Kenichi Ishibashi, Tokyo Medical and Dental
 University, 2nd Internal Medicine; yushima 1-5-45, Bunkyo, Tokyo
 113-8519, Japan (E-mail: kishibashi.med2@med.tmd.ac.jp,
 Tel:81-3-5803-5223, Fax:81-3-5803-0132)
 REFERENCE
 AUTHORS 2 (sites)
 TITLE Ishibashi, K. and Marumo, F.
 JOURNAL Molecular cloning of a DEG/ENAC sodium channel cDNA from human
 testis
 MEDLINE Biochem. Res. Commun. 245 (2), 589-593 (1998)
 FEATURES
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LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
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DEFINITION	Sequence 5 from Patent WO9854316.								
ACCESSION	A82597								
VERSION	A82597.1	GI:6732341							
KEYWORDS	human.								
ORGANISM	Homo sapiens								
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;								
AUTHORS	Mammalia: Eutheria: Primates: Catarrhini: Homiidae: Homo.								
TITLE	1 (bases 1 to 1650)								
JOURNAL	SODIUM CHANNEL RECEPTOR								
	Patent: WO 9854316-A 5 03-DEC-1998;								

GRAHAM DAVID (FR) : RENARD STEPHANE (FR)									
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Query Match	91.7%;	Score 1588.8;	DB 6;	Length 1650;					
Best Local Similarity	98.4%;	Pred. No. 8.9e-264;							
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OY	622	ACTACTAGGGGTGCATGTGGCAATGGGCTGCATCATCTGTGACGTGCAGCAGAGAGAA	681						
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LOCUS
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DEFINITION Homo sapiens acid sensing ion channel 3 splice variant c mRNA,
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ACCESSION AF195025
VERSION AF195025.1 GI:6635434
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ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1650)
AUTHORS Renard,S., Besnard,F., Partiseti,M. and Graham,D.
TITLE ASIC3c a new member of the acid sensing ion channel family
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1650)
AUTHORS Renard,S., Besnard,F., Partiseti,M. and Graham,D.
TITLE Direct Submission
JOURNAL Submitted (14-OCT-1999) Functional Genomics, Sanofi-Synthelabo, 10
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DEFINITION Homo sapiens acid sensing ion channel 3 splice variant b mRNA,
complete cds.
ACCESSION AF195024
VERSION AF195024.1 GI:6635432
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1632)
Renard,S., Besnard,F., Partiseti,M. and Graham,D.
AS1C3b a new modulatory subunit of the acid sensing ion channel
family
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1632)
Renard,S., Besnard,F., Partiseti,M. and Graham,D.
Direct Subsmission
TITLE Submitted (14-OCT-1999) Functional Genomics, Sanofi-Synthelabo, 10
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DB 63 CGGACAGAGCTGATGACAGGGGCTGGGCGACGCTTCGGGGCCAGGCGCTGAGCCTGCG 122
OY 144 CCGGGGGATGTGGGACAGCGCGCTGGTCTGTCAAGTGGCACCTTCCTTACCAGGTGCG 203
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 123 CCGGGGGATGTGGGACAGCGCGCTGGTCTGTCAAGTGGCACCTTCCTTACCAGGTGCG 182
OY 204 TGAAGAGGTGGGCTACTACAGGAGGTTCACACAGACTGGCCCTTGATGAGCAGGAAG 263
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DB 183 TGAAGAGGTGGGCTACTACAGGAGGTTCACACAGACTGGCCCTTGATGAGCAGGAAG 242
OY 264 CCACGGGCTGCTCTCCGCGCTGTCAACCTGTGCAACATCAACCCGACTGCGCGCTCGCG 323
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 243 CCACGGGCTGATCTCCGCGCTGTCAACCTGTGCAACATCAACCCGACTGCGCGCTCGCG 302
OY 324 CCTAACGCCCAAGACATGACATGGGCTGGTCTGGCTGCTGGGCTGGATCCGCGAGA 383
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DB 303 CCTAACGCCCAAGACATGACATGGGCTGGTCTGGCTGCTGGGCTGGATCCGCGAGA 362
OY 384 GCAGCGCGGCTTCCTGCGCGCGCTGGGCGCGCCCTGACCGCGCGGCTTCATGGCCAG 443
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DB 363 GCAGCGCGGCTTCCTGCGCGCGCTGGGCGCGCCCTGACCGCGCGGCTTCATGGCCAG 422
OY 444 TCCCACTTTGACATGCGCGCAACTGTATGCCCTGTGCGGCACTCCCTGATGACATGCT 503
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DB 423 TCCCACTTTGACATGCGCGCAACTGTATGCCCTGTGCGGCACTCCCTGATGACATGCT 482
OY 504 GCTGACACTGCTCCCTTCGGGCGCAACTGTGTGGGCTGGAACCTTCACACAGATCTTAC 563
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 483 GCTGACACTGCTCCCTTCGGGCGCAACTGTGTGGGCTGGAACCTTCACACAGATCTTAC 542
OY 564 CCGGATGGGAAGTGTCTACACATTTAACTCTGGCGCTGATGGGGAGAGACTCTCACAC 623
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DB 543 CCGGATGGGAAGTGTCTACACATTTAACTCTGGCGCTGATGGGGAGAGACTCTCACAC 602
OY 624 TACTAGGGGTGGCATGGGCAATGGCTGACATCATGTGGAAGCTGACAGCAGAGGAATA 683
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DB 603 TACTAGGGGTGGCATGGGCAATGGCTGACATCATGTGGAAGCTGACAGCAGAGGAATA 662
OY 684 TCTACTCTGTGTGAGAGGACATGAGAGACCCCGTTTGAAGTGGGAGATCCGAGTGCAGAT 743
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 663 TCTACTCTGTGTGAGAGGACATGAGAGACCCCGTTTGAAGTGGGAGATCCGAGTGCAGAT 722
OY 744 CCACAGCCAGAGAGAGCGCCCATCATGATGATGAGGCTTGGGGGTGTCCCGGGGCTA 803
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DB 723 CCACAGCCAGAGAGAGCGCCCATCATGATGATGAGGCTTGGGGGTGTCCCGGGGCTA 782
OY 804 CCAGACCTTTGTTTCTTGCCACAGCAGACGACTGAGCTTCTGACACCGCCCTGGGGGCA 863
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DB 783 CCAGACCTTTGTTTCTTGCCACAGCAGACGACTGAGCTTCTGACACCGCCCTGGGGGCA 842
OY 864 TTGCAATTACGATCTTGAAACCCCAACTATGAGCCAGAGCCCTGTGATCCCTAGGCTC 923

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DB 843 TTGCAATTACGATCTCTGAAACCCCAATATGAGCAGAGCCCTGTGATCCCTAGGCTC 902
OY 924 CCCCAAGCCCAAGCCCAAGCCCTCTATATACCTTATGGGTTGCTGGCTGGGGAAC 983
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DB 903 CCCCAAGCCCAAGCCCAAGCCCTCTATATACCTTATGGGTTGCTGGCTGGGGAAC 962
OY 984 CCGCTACGTTGCTGGGAAGTGGGCTGCGGATGATGATGATGATGATGATGATGATGAT 1043
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DB 963 CCGCTACGTTGCTGGGAAGTGGGCTGCGGATGATGATGATGATGATGATGATGATGAT 1022
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DB 1143 GGTGGGATCCCGAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1202
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DB 1203 GGCCTACATCGCGGAGAACGTGCTGCGCTGAGACATCTTCTTGAAGCCCTCACTATGA 1262
OY 1284 GACCGTGGAGCAGAAAGGCGCTATGAGATGACAGAGCTGTGATGATGATGATGATGAT 1343
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DB 1263 GACCGTGGAGCAGAAAGGCGCTATGAGATGACAGAGCTGTGATGATGATGATGATGAT 1322
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DB 1383 TTAGGTTTCCGAGACAAAGTCTTGGATATTTCTTGGAACGACAGCACTCCCAAGGCA 1442
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DB 1443 CTTCAGACCAATCT- 1457
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OY 1584 CCACCGACCTGCTACCTTGTACACAGACTGTAGACCTGTGTGTGTGTGTGTGTGTGTGT 1643
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LOCUS A87685
DEFINITION Sequence 5 from Patent WO9835034.
ACCESSION A87685
VERSION A87685.1 GI:6736306
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1602)
AUTHORS Heurteaux, C. and Champigny, G.
TITLE MAMMAL NEURONAL ACID SENSING CATIONIC CHANNEL. CLONING AND

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Matches 1282: Conservative 0; Mismatches 293; Indels 3; Gaps 1;				
Oy	43	GAGGAGCCCGGCGGAGCCCTGGACATCCGCTGTCCCGGAGGACGCTCGATGAC	102	
Db	25	GAGGCCCGAGCGGAGAGCCCTGACATCCGGGTGTTGGCCAGCAGTGCATGCT	84	
Oy	103	GGGCTGGGCGACGCTTGGGGCAGGAGCCCTGAGCCTGGCCGGGGGATGGGCGACG	162	
Db	85	GCTGTGGGCGACATCTTGGCCCTGGAGGCGTGCACCTGGCCGCGAGGGGTGGGCGACA	144	
Oy	163	GCCGTGGCTCTGTCAGTGGCCACTTCTCTACAGTGGCTGAGAGGGGTGGCTACTAC	222	
Db	145	GCTGTGCTCTGTCTGGTGGCTCTCTACAGTGGCTGAGCGGGTTCCTACTAT	204	
Oy	223	AGGGAGTTCACACACAGACTGCTCTGATGAGCAGAAAGCCAGCCGCTCTTCCG	282	
Db	205	GGGGAGTTCACACATAGACACCCCTGATGAGCTGAGAGCCAGCAGCTACCTTCCA	264	
Oy	283	GCTGTACCTGTGCAACATCAACCCACTGCGCGCTGCGGCTAACGCCAAGACCTG	342	
Db	265	GCTGTACTCTGTATATCAACCCACTGCGCGCTCACACGCCCTCACACCAATGACTTG	324	
Oy	343	CACGTGGGTGGTCTGGCCTGCTGGGCTGGATCCCGCAGACAGCCGCTTCTGGCG	402	
Db	325	CACGTGGGTGGAAACAGCCTGCTGGGCTGGACCTGCTGAACATGTGCTTCTCGT	384	
Oy	403	GCCCTGGGCGGCGCCCTGACACGCGCGGCTTCATGCCCAGTCCCACTTTGACATGGCG	462	
Db	385	GCACGTGGGCGAGCGCCCGGACACCTGCTTCATGCCAGTCCGACTTGTACATGGCA	444	
Oy	463	CACCTCTATGCCCGTGTGGGCGACTCCCTGGATGACATGTGCTGGACTGTGCTTCCGT	522	
Db	445	CAACCTACGCGCAGAGCGCGGCGACCTCCCTGAGGACATGTGTGATGGCGGATACCGT	504	
Oy	523	GGCCAACTGTGGGCTGAGAACTTCAACAGATCTTCAACCCGGATGGAAAGTGTAC	582	
Db	505	GGCCAGCCCTGTGGGCTGAGAACTTCAACAGTATCTTACATGATGGGCGGAAATGTAC	564	
Oy	583	ACATTTAACTGTGGGCTGATGGGCGAGAGCTGTCCACCACTACTAGGAGTGGCATGGGC	642	
Db	565	ACCTTCAACTGTGTGGGCGAGGCTGACAGGTGCTCACACACTCCAAAGGTGTGCTGGC	624	
Oy	643	AATGGGCTGACATATGCTGTGACCTGCACGACGAGAAATATCTACTGTGTGAGGAGC	702	
Db	625	AACGACTGTGAGATATCTAGATGTACAGCAAGAGAGTATCTCCATCTGGAGAGAC	684	
Oy	703	AATGAGGAGACCCGTTTGAAGTGGGATCCGAGTGCAGATCCACAGCAGAGAGAGCG	762	
Db	685	ATGGAAGAGACCCGTTTGAAGTGGGATCCGAGTGCAGATTCACAGCAGAGATAGCC	744	
Oy	763	CCCATCATCGATCAGCTGGGCTTGGGGGTGTCCCGGGCTACACAGACCTTGTCTTTC	822	
Db	745	CCTGCATTTGAACACAGCTGGGCTTGGGGCAGGCCACATCAACATTTTGTGCTGCT	804	
Oy	823	CAGCAGACGACGTGAGCTTCTGTCACCGCCCTGGGGCGATGGAGTTCAGATCTCTG	882	
Db	805	CAGCAGCAGCACTGAGTCTCTGTCACACACCTGGGGTGACTGCAATACGCAATCTTG	864	
Oy	883	AAACCCACATA--TGACCGCAGAGCCCTGTATCCCTCAAGCTCCCCAGCCCGCCAGCC	939	
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Db	925	AGCCCTCTTATAGTTTAATAGTTGTGCGCTGGGCTGTGAGTCTCGCTATGTGCTGG	984	
Oy	1000	AAGTGGGCTCCGAGATGTTTACATGCGAGCGACGTGCGATGTGCGAGCCCGCAGCAG	1059	
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Oy	1120	CCCAACCCGTGGCGGACGCGTACGCCCAAGAGCTCTCCATGTGCGGATCCCGAGC	1179
Db	1105	CCCAACCCGTGGCGGCTACTACAGCTATGCGCAAGAGCTCTCCATGTGCGGATCCCGAGC	1164
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Db	1165	CGCGCGGCTAGCTCGCTACTGTGGCCGGAAATACAAACCGCAGGAGTCTGACTTAGGAG	1224
Oy	1240	AACGTGTGGCGCTGAGACTTCTTTTGAAGCCCTCAACTATGAGACCGTGGACGAGAG	1299
Db	1225	AATGTACTGTGTCTGGATATCTTCTTGAAGCCCTCAACTATGAGACCGTGGACGAGAG	1284
Oy	1300	AAGCCTATGAGATGTACAGCTGCTTGTGATATGGGGCGACAGTGGGCTTTTTCAG	1359
Db	1285	GGCGCTATGAGATGTGCGAGCTGCTGGAGACATTTGGGGCAGACAGATGGAGCTTTAT	1344
Oy	1360	GGGCGACGCTGCTACCATCTCGAGATCTTACATCTGTGAGCTTCCGAGAC	1419
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Db	1405	AGATCTGGGATTTCTGGAACAGAGAGCGCTCAAAAGCGCTTGGCAACACTGTG	1464
Oy	1480	CTTCAGGAAGGCTGGCGAGCATGAAACCAAGTTCCCACTTCAGCTGGGCGCCAGA	1539
Db	1465	CTCCAGGAAGATTAATAGGCGATGAAACACATGTTCGCCACTCAGCTAGGGCGCAGG	1524
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DEFINITION	Sequence 7 from Patent W00181570.			
ACCESSION	AX286638			
VERSION	AX286638.1 GI:17048711			
KEYWORDS				
SOURCE	Rattus sp.			
ORGANISM	Rattus sp.			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;			
TITLE	Rattus.			
JOURNAL	Seguela P. and Babinski K.			
FEATURES	Heteromultimeric ion channel receptor and uses thereof			
source	Patent: WO 0181570-A 7 01-NOV-2001;			
	McGILL UNIVERSITY (CA)			
	Location/Qualifiers			
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Best Local Similarity 81.2%; Pred. No. 4.3e-179;				
Matches 1282; Conservative 0; Mismatches 293; Indels 3; Gaps 1;				
Oy	43	GAGGAGCCCGGCGGAGCCCTGCGACATCCGCTGTTCGCGACCAACTGCTGCATGCAC	102	
Db	25	GAGGCCCGAGCGGCGAGCCCTGACATCCGGGTGTTGGCCAGCAGTGCATGCTCAT	84	
Oy	103	GGGCTGGGCGACGCTTGGGGCAGGAGCCCTGAGCCTGGCCGGGGGATGGGCGACG	162	
Db	85	GCTGTGGGCGACATCTTGGCCCTGGAGGCGTGCACCTGGCCGCGAGGGGTGGGCGACA	144	

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Db 85 GGTGTGGCCACATCTTTGGCCCTGGAGGCTTGACCTGCGCCGAGGCTGTGGCCACA 144
QY 163 GCGGTGTCCTGTCACTGTGGCCACCTTCCTACACAGTGGCTGAGAGGTTGGCTACTAC 222
Db 145 GCTGTGCTCTGTGCTGGCGGCTCTCTACACAGTGGCTGAGGCTGGCTCTACTAT 204
QY 223 AGGAGTTCACACACACAGTGGCTGATGAGCGAGAAAGCCAGGCTGCTGCTCCG 282
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QY 283 GCTGTACCCCTGTGCAACATCAACCCATGCGCGGCTGCGCCCTAACGCCCAAGACTG 342
Db 265 GCTGTACTCTGTATATCAACCCATGCGCGGCTGACGCTCAGCCCAACCAATGACTTG 324
QY 343 CACTGGGCTGGGCTGCTGCTGCTGGCTGTGATCCCGAGAGACGCGCTTCTGCGCG 402
Db 325 CACTGGGCTGGGAACACGCGTGTGGGCTGTGACCCCTGTGAACATCTGCTACCTTCGT 384
QY 403 GCGCTGGGCGGCGCCCTGACCGCGCGGCTTCATGCTCCAGTCCACCTTTGACATGGG 462
Db 385 GCACTGTGGCCAGCCCCCGCACCTGCTTCATGCTCCAGTCCAGCTTTGACATGGCA 444
QY 463 CAACTGTATCCCGTGTGGGCACTCCCTGTGATGACATGCTGTGACTGTGCTTCGCT 522
Db 445 CAACTGTACGCAAGACCGGCACTCCCTGTGAGAGATGTGTGATGGCCATTCGCT 504
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Db 505 GCGCAACCTTGTGGGCTGTGAGAACTTACAGATTTTACTGGAATGGGCAATCTAC 564
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Db 565 ACCTTCACTGTGTGTGCTCCACGCTGTGAGAGTGTGTCTACCACTTCAAGGCTGTGCTGG 624
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QY 703 AATGAGAGAACCCCGTTTGAAGTGGGATCCGAGTGCATTCACAGCCAGAGAGCCG 762
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Db 1285 GCGGCTTATGAAATGTGTGAGAGTGTGTGAGACATTTGGGCGCAGATGGGACTTTTATTT 1344
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Search completed: October 11, 2002, 03:45:58
 Job time : 3225 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2002, 02:43:14 ; Search time 284 Seconds
(without alignments)
10470.760 Million cell updates/sec

Title: US-09-530-233-1

Perfect score: 1732
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1732	100.0	1732	24	AA517126
3	1715.2	99.0	1736	21	AAZ61203
4	1588.8	91.7	1650	20	AAV84191
5	1583.8	91.4	1723	20	AAV84189
6	1508.2	87.1	1711	20	AAV84190
7	1096.4	63.3	1602	19	AAV60843
8	1096.4	63.3	1602	21	AAZ61201
9	1096.4	63.3	1602	24	AA517128

10	472.2	27.3	2962	20	AA528161
11	470.6	27.2	3647	19	AAV60842
12	470.6	27.2	3647	21	AAZ61200
13	456.8	26.4	1620	19	AAV60840
14	456.8	26.4	1620	21	AAZ61198
15	453.2	26.2	3562	19	AAV60839
16	453.2	26.2	3562	21	AAZ61197
17	423.2	24.4	2711	19	AAV68056
18	421	24.3	2528	22	AAV68056
19	420.6	24.3	1632	19	AAV68059
20	416.2	24.0	1666	21	AAV60841
21	416.2	24.0	1666	21	AAZ61199
22	416.2	24.0	2565	24	AA517127
23	415.8	24.0	1539	20	AA523167
24	415.8	24.0	2748	24	AA517125
25	391.4	22.6	2622	21	AAZ36802
26	352.2	20.3	1948	19	AAV60844
27	352.2	20.3	1948	21	AAZ61202
28	288.6	16.7	2955	19	AAV68057
29	246.8	14.2	1203	21	AA59324
30	246.8	14.2	2516	21	AA59323
31	191	11.0	192	24	AA517133
32	174	10.0	960	20	AA528162
33	170.4	9.8	451	22	ABA13241
34	170.4	9.8	451	22	AA162780
35	165.2	9.5	508	19	AAV68058
36	148.8	8.6	152	24	AA517137
37	99	5.7	354	22	AAH35552
38	91.6	5.3	444	22	AAK31936
39	87.8	5.1	271	22	AA137802
40	87.8	5.1	271	22	ABA70302
41	87.8	5.1	271	22	AAK18532
42	87.8	5.1	271	22	AAK44449
43	87.8	5.1	271	22	AA150442
44	78.2	4.5	490	22	ABA57682
45	78.2	4.5	490	22	AAK05740

ALIGNMENTS

RESULT 1	AA56237	standard; DNA; 1732 Bp.
ID	AA56237;	
AC	AA56237;	
XX		
DT	16-JUL-1999	(first entry)
XX		
DE	Human proton-gated cation channel encoding DNA.	
XX		
KW	Human; non-inactivating amiloride-sensitive proton-gated cation channel;	
KW	hASIC3; analgesic; ss.	
XX		
OS	Homo sapiens.	
XX		
FT	key	Location/Qualifiers
FT	CDS	22..1617
FT		/tag= a
PN	W09921981-A1.	
XX		
PD	06-MAY-1999.	
XX		
PF	29-OCT-1998;	98WO-CA01016.
XX		
PR	29-OCT-1997;	97CA-2219713.
XX		
PA	(UYMC-) UNITV MCGILL.	
XX		
PI	Babinski K, Seguela P;	
XX		
DR	WPI; 1999-312958/26.	

Rat Acid sensitive
Rat acid sensing i
cDNA encoding a ra
Partial human acid
cDNA encoding a pa
Rat acid sensing i
cDNA encoding a ra
Neurodegenerative
Human brain sodium
Neurodegenerative
Human acid sensing
cDNA encoding a hu
Rat cDNA encoding
Human BNC1 cDNA.
Human cDNA encodin
Nucleic acid encod
Rat acid sensing i
cDNA encoding a ra
Neurodegenerative
Coding region of a
DNA encoding a hum
Human cDNA encodin
Rat Acid sensitive
Human nervous syst
Human cDNA SEQ ID
Neurodegenerative
Human cDNA encodin
Human colon cancer
Human bone marrow
Probe #6488 used t
Human brain expres
Human bone marrow
Probe #19128 used
Human foetal liver
Human brain expres

DR P-PSDB; AA09509.

XX Use of human protein as a proton-gated cation channel

PS Claim 1; Fig 1; 32pp; English.

XX The present sequence encodes a human non-inactivating amiloride-sensitive
CC proton-gated cation channel designated hASIC3. hASIC3, its encoding
CC nucleic acid and the recombinant host cell are useful in a composition
CC or a kit for screening compounds useful as proton-gated cation channel
CC ligands. The ligands are useful as analgesics.

XX Sequence 1732 BP; 326 A; 601 C; 484 G; 321 T; 0 other:

Query Match 100.0%; Score 1732; DB 20; Length 1732;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1732: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 TCGCAGCAGCGGTTCTGGCCATGAAGCCACCTCAGGCCAGAGAGGCCGGGGCAG 60
DB 1 TCGCAGCAGCGGTTCTGGCCATGAAGCCACCTCAGGCCAGAGAGGCCGGGGCAG 60
OY 61 CCGTGGGACATCCGGCTGTCTCCAGCAACTGCTGATGCAGGGCTGGGCCACTTTC 120
DB 61 CCGTGGGACATCCGGCTGTCTCCAGCAACTGCTGATGCAGGGCTGGGCCACTTTC 120
OY 121 GGGCCAGCAGCCTGAGCCTGCGCGGGGATGTGGGAGCGGCGCTGTCTCAGTG 180
DB 121 GGGCCAGCAGCCTGAGCCTGCGCGGGGATGTGGGAGCGGCGCTGTCTCAGTG 180
OY 181 GCCACCTTCTTACCAAGGTGCTGAGAGGGTGCCTACTACAGGAGTTCCACACAGC 240
DB 181 GCCACCTTCTTACCAAGGTGCTGAGAGGGTGCCTACTACAGGAGTTCCACACAGC 240
OY 241 ACTGCCCTGATGAGCAGAAAGCCACCGGCTGCTTCCGGGCTGACACCTGTGCAAC 300
DB 241 ACTGCCCTGATGAGCAGAAAGCCACCGGCTGCTTCCGGGCTGACACCTGTGCAAC 300
OY 301 ATCAACCCCACTGCGCGCTGCGCCTAAACGCCCAACGACTTGCAGTGGGCTGTGCG 360
DB 301 ATCAACCCCACTGCGCGCTGCGCCTAAACGCCCAACGACTTGCAGTGGGCTGTGCG 360
OY 361 CTGCTGGGCTGTGATCCCGCAGAGCAAGCGGCTTCTGCGGCGCTGGGGCCCTCT 420
DB 361 CTGCTGGGCTGTGATCCCGCAGAGCAAGCGGCTTCTGCGGCGCTGGGGCCCTCT 420
OY 421 GCACCGCCCGGCTTATGCGCCAGTCCCACTTTCAGATGGGCAACTGATGCCGTGT 480
DB 421 GCACCGCCCGGCTTATGCGCCAGTCCCACTTTCAGATGGGCAACTGATGCCGTGT 480
OY 481 GGGCAGCTCCCTGATGATGCTGTGACTGTGCGCTTCCGTGGCAACTTGTGGGCT 540
DB 481 GGGCAGCTCCCTGATGATGCTGTGACTGTGCGCTTCCGTGGCAACTTGTGGGCT 540
OY 541 GAGAACTTCACACAGATCTTCAACCGGATGGGAAAGTCTACACTTAACTTGGCCCT 600
DB 541 GAGAACTTCACACAGATCTTCAACCGGATGGGAAAGTCTACACTTAACTTGGCCCT 600
OY 601 GATGGGAGAGAGCTCTACCACTACTAGGGGTGSCATGGCAATGGGCTGGACATCATG 660
DB 601 GATGGGAGAGAGCTCTACCACTACTAGGGGTGSCATGGCAATGGGCTGGACATCATG 660
OY 661 CTGACGTGACAGAGAGAAATATCTACCTGTGTGAGGAGCAATGAGAGACCCCGTTT 720
DB 661 CTGACGTGACAGAGAGAAATATCTACCTGTGTGAGGAGCAATGAGAGACCCCGTTT 720
OY 721 GAGTGGGGGATCCGAGTGCAGATCCACAGCAGAGAGGCCGCCATATGATAGCTG 780
DB 721 GAGTGGGGGATCCGAGTGCAGATCCACAGCAGAGAGGCCGCCATATGATAGCTG 780
OY 781 GCGTTGGGGGTGTCGCCGGGTACAGAGACTTTGTTCTTGGCAGCAGCAGAGCTGAGC 840
DB 781 GCGTTGGGGGTGTCGCCGGGTACAGAGACTTTGTTCTTGGCAGCAGCAGAGCTGAGC 840
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OY 841 TTCTGCGCACCGCCCTGGGGCGATTGCAAGTTCAGACTCTGAAACCCCACTATGAGCCA 900
DB 841 TTCTGCGCACCGCCCTGGGGCGATTGCAAGTTCAGACTCTGAAACCCCACTATGAGCCA 900
OY 901 GAGCCCTCTGATCCCTTAGGCTTCCCCAGACCCCAAGCCCAAGCCCTCTATACCTTATG 960
DB 901 GAGCCCTCTGATCCCTTAGGCTTCCCCAGACCCCAAGCCCAAGCCCTCTATACCTTATG 960
OY 961 GGGTGTGCGGTGGGCTGGGAAACCCGCTACGAGGCTGGGAAAGTGGGCGGAAATGCTG 1020
DB 961 GGGTGTGCGGTGGGCTGGGAAACCCGCTACGAGGCTGGGAAAGTGGGCGGAAATGCTG 1020
OY 1021 TACATGCCAGGCGAGCTGCTCAGTGTGCAGCCGCCAGCAGTACAGAACTGTGCCACCG 1080
DB 1021 TACATGCCAGGCGAGCTGCTCAGTGTGCAGCCGCCAGCAGTACAGAACTGTGCCACCG 1080
OY 1081 GCCATAGATGCCATCTTTCGCAAGGACTGTGCGCTGCCAACCCTGTGCCAGCAGC 1140
DB 1081 GCCATAGATGCCATCTTTCGCAAGGACTGTGCGCTGCCAACCCTGTGCCAGCAGC 1140
OY 1141 CCGTACGCCAAGAGACTGCTCCATGCTGGGATCCCGAGCGCGCGCGCGCTTCTCTG 1200
DB 1141 CCGTACGCCAAGAGACTGCTCCATGCTGGGATCCCGAGCGCGCGCGCGCTTCTCTG 1200
OY 1201 GCCCGAAGCTCAACCGCAGAGGCTTACATCCGCGAGAAAGTGTGGCCCTGGACATC 1260
DB 1201 GCCCGAAGCTCAACCGCAGAGGCTTACATCCGCGAGAAAGTGTGGCCCTGGACATC 1260
OY 1261 TTTCTTGAAGCCCTCACTATGAGACCGTGTGAGCAGCAAGAAAGCCCTATGAGATGTGAG 1320
DB 1261 TTTCTTGAAGCCCTCACTATGAGACCGTGTGAGCAGCAAGAAAGCCCTATGAGATGTGAG 1320
OY 1321 CTGCTTGTGATTTGGGGGCGAGATGGGCGCTTTCATCGGGGCGAGCTGCTCAACATC 1380
DB 1321 CTGCTTGTGATTTGGGGGCGAGATGGGCGCTTTCATCGGGGCGAGCTGCTCAACATC 1380
OY 1381 CTGAGATCTTAGACTTCTGTGAGGTGTTCGAGACAAAGTCTGGGATATTCTGCG 1440
DB 1381 CTGAGATCTTAGACTTCTGTGAGGTGTTCGAGACAAAGTCTGGGATATTCTGCG 1440
OY 1441 AACCGACAGCACTCCCAAGGACCTCCAGCAACCAATGCTTTCAGAGAAAGGCTGGGCAAC 1500
DB 1441 AACCGACAGCACTCCCAAGGACCTCCAGCAACCAATGCTTTCAGAGAAAGGCTGGGCAAC 1500
OY 1501 CATGGAACCAAGTTCGCCACCTCAGCCTGGGCGCCAGACCTCCACACCCCTCGTGGCC 1560
DB 1501 CATGGAACCAAGTTCGCCACCTCAGCCTGGGCGCCAGACCTCCACACCCCTCGTGGCC 1560
OY 1561 GTCAACCAAGACTTCTCCGCTCCACACGCACTGTACTTGTACACAGCTCTAGACC 1620
DB 1561 GTCAACCAAGACTTCTCCGCTCCACACGCACTGTACTTGTACACAGCTCTAGACC 1620
OY 1621 TGTCTGTGTGTCTCTCGAGAGCCCGCCCTGACATCTGGAATGCTCTGACAGCTAG 1680
DB 1621 TGTCTGTGTGTCTCTCGAGAGCCCGCCCTGACATCTGGAATGCTCTGACAGCTAG 1680
OY 1681 CTTTTCCTCTTCAACCCCAATTAAGTCTTAATGCATCAAAAAAAAAAAAAA 1732
DB 1681 CTTTTCCTCTTCAACCCCAATTAAGTCTTAATGCATCAAAAAAAAAAAAAA 1732

RESULT 2
AA09509
ID AA09509 standard; cDNA; 1732 BP.
XX
XX AA09509:
XX
XX 14-FEB-2002 (first entry)
XX
XX Human cDNA encoding acid sensing ion channel subunit 3, ASIC3A.
XX
XX Human; ss: acid sensing ion channel; ASIC3A; analgesic; anti-HIV;
KW
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neuroprotective; nootropic; antiparkinsonian; anticonvulsant;
cerebroprotective; cardiact; antilanginal; hypotensive;
antithrombotic; vasotropic; tranquilizer; antidepressant;
chronic pain; neuropathic pain; diabetes; cancer; AIDS;
acquired immunodeficiency syndrome; neurodegenerative disease;
Alzheimer's disease; Parkinson's disease; Huntington's disease;
Creutzfeldt-Jacob disease; amyotrophic lateral sclerosis; dementia;
convulsion; epilepsy; stroke; anxiety; depression; angina;
cardiovascular disease; congestive heart failure; vasoconstriction;
hypertension; atherosclerosis; restenosis; bleeding; gene therapy.

Homo sapiens.

Key Location/Qualifiers
CDS 22..1617
FT /tag-a
FT /product= "ASIC3A"

WO200181570-A2.
01-NOV-2001.
20-APR-2001; 2001WO-CA00561.
20-APR-2000; 2000CA-2304494.
(UWMC-) UNIV MCGILL.
Seguela P, Babiniski K;
WPI: 2002-055353/07.
P-PSDB: AAU10904.

New heteromultimeric proton-gated ion channel for diagnosing, treating
diseases associated with expression of the channel e.g.
neurodegenerative diseases, comprises two different types of acid
sensing ion channel subunits

Claim 7; Page 96-97; 105pp; English.

The invention relates to a protein complex forming a heteromultimeric
amiloride- and gadolinium-sensitive proton-gated cation channel
(ASIC-2S.2), where the individual components of the heteromultimeric
channel include the acid sensing ion channel (ASIC2A and ASIC3 protein
or their variants having 80% sequence identity, the channel being
activated by protons, acids, low pH solutions, the nucleic acids
encoding the subunits, a recombinant bicistronic vector comprising a
nucleic acid encoding at least two individual subunits or variants of
ASIC-2S.2, a host cell comprising the vector, an antibody raised against
one of the subunits or a domain which is capable of disrupting assembly
of the ion channel and ant/agonists of the ion channel. The polypeptides
and polynucleotides are useful for diagnosing a disease or a
susceptibility to a disease in a subject related to expression or
activity of the heteromultimeric channel (e.g. by gene therapy using the
vector). Such diseases include chronic pain, neuropathic pain such as
diabetic-, cancer- and AIDS (acquired immunodeficiency syndrome)-related,
neurodegenerative diseases such as Alzheimer's disease, Parkinson's
disease, Huntington's disease, Creutzfeldt-Jacob disease, and amyotrophic
lateral sclerosis and dementias, including AIDS-related as well as
convulsions, epilepsy, stroke, anxiety and depression. They are also
useful for treating cardiovascular diseases such as angina, congestive
heart failure, vasoconstriction, hypertension, atherosclerosis,
restenosis and bleeding. ASIC-2S.2 plays a role in the regulation of
neurotransmitter release, neuronal excitability or excitotoxicity and is
useful in screening for compounds that regulate neurotransmitter release,
CC synaptic efficacy, neuroexcitability or neurotoxicity. The present
sequence encodes human ASIC3A.

Sequence 1732 BP; 326 A; 601 C; 484 G; 321 T; 0 other;

Query Match 100.0%; Score 1732; DB 24; Length 1732;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1732; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TCGCAGCAGCGGCTTCTGGCCATGAAGCCCACTCAGGCCAGAGAGGCGCGGGCAG 60
1 TCGCAGCAGCGGCTTCTGGCCATGAAGCCCACTCAGGCCAGAGAGGCGCGGGCAG 60
61 CCTCGGACATCGCGCTGTTCGACCACTCTGCATCAGAGGCGTGGCCACGCTTTC 120
61 CCTCGGACATCGCGCTGTTCGACCACTCTGCATCAGAGGCGTGGCCACGCTTTC 120
121 GGGCCAGCAGCCTGAGCCTGCGCGGGGAGTGTGGGCAAGCGGCGTGTCTGTACGTG 180
121 GGGCCAGCAGCCTGAGCCTGCGCGGGGAGTGTGGGCAAGCGGCGTGTCTGTACGTG 180
181 GGCACCTTCTCTACCAAGGTGGGTGAGAGGTTGCGCTACTACAGGAGTTCACACCCAG 240
181 GGCACCTTCTCTACCAAGGTGGGTGAGAGGTTGCGCTACTACAGGAGTTCACACCCAG 240
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241 ACTGCCCTGGATGAGCGAGAAAGCCACCGGCTCGTCTCCGGCTGTCAACCTGTGCAAC 300
301 ATCAACCCACTGCGCGCTGCGGCTTAACGCCCAACGACCTGCACTGGGCTGTGCG 360
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361 CTGCTGGGCTGGATTCGGCAGAGCAGCGCGCTTCTGCGGCGCGCGCGCGCT 420
361 CTGCTGGGCTGGATTCGGCAGAGCAGCGCGCTTCTGCGGCGCGCGCGCGCT 420
421 GCACCGCGCGCTTCATGCGCCAGTCCACCTTTCGATGAGCGCAATCTATGCGCTGT 480
421 GCACCGCGCGCTTCATGCGCCAGTCCACCTTTCGATGAGCGCAATCTATGCGCTGT 480
481 GGGCACTCCCTGGATGATGCTGTGACCTGTGCTTCTGCGGCACTTGTGGGCT 540
481 GGGCACTCCCTGGATGATGCTGTGACCTGTGCTTCTGCGGCACTTGTGGGCT 540
541 GAGAACTTACCAACGATCTTTCACCGGATGGGAAATGCTTACCAATTAATCTGGCGCT 600
541 GAGAACTTACCAACGATCTTTCACCGGATGGGAAATGCTTACCAATTAATCTGGCGCT 600
601 GATGGGCGAGAGTGTCTACCACTACTAGGAGGATGGGATGGGCTGACATCATG 660
601 GATGGGCGAGAGTGTCTACCACTACTAGGAGGATGGGATGGGCTGACATCATG 660
661 CTGACGTGCAGCAGAGGAAATATCTACTGTGTGAGGAGACATGAGAGACCCGTTT 720
661 CTGACGTGCAGCAGAGGAAATATCTACTGTGTGAGGAGACATGAGAGACCCGTTT 720
721 GAGGTGGGATCCGATGCAATCCACAGCCAGGAGAGCGCGCCATCAATCAATCAGCTG 780
721 GAGGTGGGATCCGATGCAATCCACAGCCAGGAGAGCGCGCCATCAATCAATCAGCTG 780
781 GGGTGGGAGTGTCCCGGGGCTACAGACCTTGTGTTTTCGACAGAGAGAGCTGAGC 840
781 GGGTGGGAGTGTCCCGGGGCTACAGACCTTGTGTTTTCGACAGAGAGAGCTGAGC 840
841 TTCTCTCCACCGCGCTGGGGGATTCAGATTCATCTGTAACCCCAATATGAGCCA 900
841 TTCTCTCCACCGCGCTGGGGGATTCAGATTCATCTGTAACCCCAATATGAGCCA 900
901 GAGCCTTGATTCCTTAGGCTTCCCGACCCAGCCCAAGCCCTTCCATACCTTATG 960
901 GAGCCTTGATTCCTTAGGCTTCCCGACCCAGCCCAAGCCCTTCCATACCTTATG 960
961 GAGCCTTGATTCCTTAGGCTTCCCGACCCAGCCCAAGCCCTTCCATACCTTATG 960
961 GAGCCTTGATTCCTTAGGCTTCCCGACCCAGCCCAAGCCCTTCCATACCTTATG 960
961 GGGTGTGCGCTGGCTGCGAAACCGCTACGTGAGTGGAGTGGGCTGCGAATGATG 1020
961 GGGTGTGCGCTGGCTGCGAAACCGCTACGTGAGTGGAGTGGGCTGCGAATGATG 1020
1021 TACATGCCAGGCGAGCTGACAGTGTGACAGCCCAACAGTACAAAGATGTGCCACCG 1080
1021 TACATGCCAGGCGAGCTGACAGTGTGACAGCCCAACAGTACAAAGATGTGCCACCG 1080

QY	1081	GCCTAGATGCACTCTTCCCAAGGACTGTGGCCCTGGCCCAACCCGTCGACAGACG	1140
QY	1081	GCCTAGATGCACTCTTCCCAAGGACTGTGGCCCTGGCCCAACCCGTCGACAGACG <td>1140</td>	1140
Db	1081	GCCTAGATGCACTCTTCCCAAGGACTGTGGCCCTGGCCCAACCCGTCGACAGACG	1140
QY	1141	CGCTACGCGCAAGAGCTCTCCATGCTGGGATCCGAGCCGCGCGCGCGCTTCTCG	1200
Db	1141	CGCTACGCGCAAGAGCTCTCCATGCTGGGATCCGAGCCGCGCGCGCGCGCTTCTCG	1200
QY	1201	GCCCGGAAGCTCAACCGCACAGAGGCTCATCTGCGGAAGAGTCTGTGCTGTGACATC	1260
Db	1201	GCCCGGAAGCTCAACCGCACAGAGGCTCATCTGCGGAAGAGTCTGTGCTGTGACATC	1260
QY	1261	TTCTTTTAGAGCCCTCAACTGTGAGACCGTGGAGACAAGAAAGCCCTATGAGATGTCAAG	1320
Db	1261	TTCTTTTAGAGCCCTCAACTGTGAGACCGTGGAGACAAGAAAGCCCTATGAGATGTCAAG	1320
QY	1321	CTGCTTGGTGACATTTGGGGGCCGATGGGCTTTTTCATCGGGGCCAGCCTGCTCACATC	1380
Db	1321	CTGCTTGGTGACATTTGGGGGCCGATGGGCTTTTTCATCGGGGCCAGCCTGCTCACATC	1380
QY	1381	CTCAGATCCAGACTCTCTGCTGAGAGGTTCGAGACAAAGTCTTGAGATATTCTGG	1440
Db	1381	CTCAGATCCAGACTCTCTGCTGAGAGGTTCGAGACAAAGTCTTGAGATATTCTGG	1440
QY	1441	AACCGACAGCACTGCCAAAGGCACTCCAGACCAATCTGCTTACAGAAAGGCTGGGACG	1500
Db	1441	AACCGACAGCACTGCCAAAGGCACTCCAGACCAATCTGCTTACAGAAAGGCTGGGACG	1500
QY	1501	CATGGAACCCAAAGTTCGCCCACTCAGCGTGGGGCCGAGACCTCCACCCCTCCGTGAC	1560
Db	1501	CATGGAACCCAAAGTTCGCCCACTCAGCGTGGGGCCGAGACCTCCACCCCTCCGTGAC	1560
QY	1561	GTCACCAAGACTCTCTCCGCTCCACACGCACTGCTACTTGTGCACACAGCTTAGAC	1620
Db	1561	GTCACCAAGACTCTCTCCGCTCCACACGCACTGCTACTTGTGCACACAGCTTAGAC	1620
QY	1621	TGCTGTGTGTCTCTGGAGCCCGCGCCCTGACATCTGTGACATGCTGAGCTGACAGTAG	1680
Db	1621	TGCTGTGTGTCTCTGGAGCCCGCGCCCTGACATCTGTGACATGCTGAGCTGACAGTAG	1680
QY	1681	CTTTTCGCTTCCACCCCAATTAAGTCTTAATGATCATCAAAAAAAAAAAAAA	1732
Db	1681	CTTTTCGCTTCCACCCCAATTAAGTCTTAATGATCATCAAAAAAAAAAAAAA	1732
RESULT 3			
AAZ61203			
ID	AAZ61203 standard; cDNA: 1736 BP.		
XX	AAZ61203:		
AC			
XX			
DT	30-MAY-2000 (first entry)		
XX			
DE	cDNA encoding a human acid-sensitive cationic channel 3 (hASIC3).		
XX			
KM	Neuronal acid-sensitive cation channel; ASIC; ASIC 3;		
KW	proton-gated cation channel; biophysical desensitization; amiloride;		
KM	cation transport channel; acid sensor; pH detection; ds.		
XX			
OS	Homo sapiens.		
XX			
FT	Key		
FT	CDS		
FT	18..1613		
FT	/tag= a		
FT	/product= "acid-sensitive cationic channel 3"		
XX	WO200008149-A2.		
PN	17-FEB-2000.		
XX			
PD	05-AUG-1999: 99MO-IB01445.		
XX			
PF	05-AUG-1998: 98US-0095408.		
XX			
PR			

xx	(CNRS) CNRS CENT NAT RECH SCI.
PA	
XX	
PI	Waldmann R, Bassilana F, Lazdunski M, De Weille JR;
XX	
DR	WPI; 2000-195574/17.
DR	P-PSDB; AAY69181.
xx	
PT	Novel human cation transport protein, Acid Sensing Ionic Channel 3 used
PT	to identify substances capable of modulating cation transport channel
XX	activity -
XX	
PS	Claim 3; Page 83; 84pp; English.
xx	
CC	The present sequence encodes a human neuronal acid-sensitive cation
CC	channel 3 (ASIC3) protein. The protein is a proton-gated cation
CC	channel subunit that has biphasic desensitisation kinetics with both
CC	a rapidly inactivating sodium-selective and a sustained component. The
CC	channels are sensitive to amiloride. The specification describes ASIC3
CC	proteins, which are expressed in the sensory neurons but not in the
CC	brain. The cation transport channel proteins can be used in methods to
CC	identify substances capable of modulating the activity of cation
CC	transport channels. The human ASIC3 protein is also an acid sensor,
CC	and might play an important role in the detection of lasting pH changes
CC	in humans.
CC	
SQ	Sequence 1736 BP; 335 A; 596 C; 486 G; 319 T; 0 other:
	Query Match 99.0%; Score 1715.2; DB 21; Length 1736;
	Best Local Similarity 99.5%; Pred. No. 0;
	Matches 1720; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
OY	5 ACGAGCGGTTCTGGCCATGAAGCCACCTCAGGCCAGAGAGGAGCCGGCGGACGCCT 64
Db	1 ACGAGCGGTTCTGGCCATGAAGCCACCTCAGGCCAGAGAGGAGCCGGCGGACGCCT 60
OY	65 CGGACATCCGCGTGTTCGCCACCAACTGCTGATCACAGGCGTGCGGCCAAGCTTCGGGC 124
Db	61 CGGACATCCGCGTGTTCGCCACCAACTGCTGATCACAGGCGTGCGGCCAAGCTTCGGGC 120
OY	125 CAGGAGCGCTGAGCGTCGGCCGGGGATGTGGGACAGGGCCGTGGTCTGTCAATGGCCA 184
Db	121 CAGGAGCGCTGAGCGTCGGCCGGGGATGTGGGACAGGGCCGTGGTCTGTCAATGGCCA 180
OY	185 CCTTCTCTTACCAGGTGGCTGAGAAGGTGGCTACTACAGGAGATTCCACACAGACTG 244
Db	181 CCTTCTCTTACCAGGTGGCTGAGAAGGTGGCTACTACAGGAGATTCCACACAGACTG 240
OY	245 CCCTGATGAGGAGAAAGAACACCGGGTCGTTCCTCCGGCTCATCCCGTGCACATCA 304
Db	241 CCCTGATGAGGAGAAAGAACACCGGGCTCATCTTCCGGCTCATCCCGTGCACATCA 300
OY	305 ACCCACTGCGCGCTCGCGCTTAACGCCCAACGACTGTGAGGCTGGGCTGGCTGC 364
Db	301 ACCCACTGCGCGCTCGCGCTTAACGCCCAACGACTGTGAGGCTGGGCTGGCTGC 360
OY	365 TGGGCGCTGGATCCGCGAAGACGCGCGCTTCCTCGGCGGCGGCGGCCCCCTGGAC 424
Db	361 TGGGCGCTGGATCCGCGAAGACGCGCGCTTCCTCGGCGGCGGCGGCCCCCTGGAC 420
OY	425 GGCGCGGCTTCATGCGCCAGTCCACCTTTGACATGGCCAACTCATGCGCCGTGGGC 484
Db	421 GGCGCGGCTTCATGCGCCAGTCCACCTTTGACATGGCCAACTCATGCGCCGTGGGC 480
OY	485 ACTCCCTGGATGACATGCTGCTGGACTGTGCTTCCGTGGCCAACTTGTGGGCTTGAGA 544
Db	481 ACTCCCTGGATGACATGCTGCTGGACTGTGCTTCCGTGGCCAACTTGTGGGCTTGAGA 540
OY	545 ACTTACACACGATCTTTCACCCGGATGGGAAAGTGTACACATTTAACTGTGGCGTGTAG 604
Db	541 ACTTACACACGATCTTTCACCCGGATGGGAAAGTGTACACATTTAACTGTGGCGTGTAG 600
OY	605 GGGCAGACTGCTCTACCACTACTAGGGGTGGCATGGGCAATGGCGTGACATCATGCTGG 664

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Db 601 GGGCAGAGCTGCTACCACTACTAGGGGTGGCATGGCAATGGGCTGGACATCATGCTGG 660
OY 665 ACGTCACACGAGAGAAATATCTACTGTGTGTGAGAGACAAATAGAGAGACCCGTTTGAGG 724
Db 661 ACGTCACACGAGAGAAATATCTACTGTGTGTGAGAGACAAATAGAGAGACCCGTTTGAGG 720
OY 725 TGGGATCCGATGAGATCCACAGCCAGAGAGAGCCGCCCTCATGATGAGTGGGCT 784
Db 721 TGGGATCCGATGAGATCCACAGCCAGAGAGAGCCGCCCTCATGATGAGTGGGCT 780
OY 785 TGGGGGTGTCCCGGGGTACAGACCTTTGTTTCTTGCCAGCAGCAGCAGTGTTC 844
Db 781 TGGGGGTGTCCCGGGGTACAGACCTTTGTTTCTTGCCAGCAGCAGCAGTGTTC 840
OY 845 TGCCACCCGCTGGGGGCAATTCAGATGACATCTGTGAAACCCCAATATGAGCCAGAGC 904
Db 841 TGCCACCCGCTGGGGGCAATTCAGATGACATCTGTGAAACCCCAATATGAGCCAGAGC 900
OY 905 CCTGTATCCCTTAGGTCGCCCAAGCCGAGCCGAGCCCTCATACCTTATGGGGT 964
Db 901 CCTGTATCCCTTAGGTCGCCCAAGCCGAGCCGAGCCCTCATACCTTATGGGGT 960
OY 965 GTCCGCTGGCCCTGCGAAACCCGCTACGTGGCTCGGAAAGTGGGCTGCCGATGTGTACA 1024
Db 961 GTCCGCTGGCCCTGCGAAACCCGCTACGTGGCTCGGAAAGTGGGCTGCCGATGTGTACA 1020
OY 1025 TGCCAGGCGACGTGCGACGTGTGACAGCCGCCAGCAGTACAGAACTGTGCCACCCGGCCA 1084
Db 1021 TGCCAGGCGACGTGCGACGTGTGACAGCCGCCAGCAGTACAGAACTGTGCCACCCGGCCA 1080
OY 1085 TAGATGCCATCCTTGTGCAAGAGATCTGTGGCTGGCCCAACCCGTGGCGACAGCGCT 1144
Db 1081 TAGATGCCATCCTTGTGCAAGAGATCTGTGGCTGGCCCAACCCGTGGCGACAGCGCT 1140
OY 1145 ACGCCAAAGAGCTTCATGTGTGCGATGCCAGCGCGCCGCGGCGCTTCTGGGCC 1204
Db 1141 ACGCCAAAGAGCTTCATGTGTGCGATGCCAGCGCGCCGCGGCGCTTCTGGGCC 1200
OY 1205 GGAAGCTCAACCGCAGCAGAGGCTTACATGCGCGAGAGACGTGTGGCCCTGTGACATCTTCT 1264
Db 1201 GGAAGCTCAACCGCAGCAGAGGCTTACATGCGCGAGAGACGTGTGGCCCTGTGACATCTTCT 1260
OY 1265 TTGAGGCTCAACATATAGAACCGTGGAGCAGAAAGAGCCCTATAGATGTAGAGCTGC 1324
Db 1261 TTGAGGCTCAACATATAGAGCTGTGGAGCAGAAAGAGCCCTATAGATGTAGAGCTGC 1320
OY 1325 TTGTGACATTTGGGGGCGAGATGGGCTTTTCATGCGGGCGAGCTGTGCTACATCTCTG 1384
Db 1321 TTGTGACATTTGGGGGCGAGATGGGCTTTTCATGCGGGCGAGCTGTGCTACATCTCTG 1380
OY 1385 AGATCTTAGACTACTCTGTGTGAGTGTTCGAGACAAAGTCTGTGGATATTTCTGGAACC 1444
Db 1381 AGATCTTAGACTACTCTGTGTGAGTGTTCGAGACAAAGTCTGTGGATATTTCTGGAACC 1440
OY 1445 GACACACTTCCCAAGGACATTCACACCAATCTGCTTACAGAAAGGCTGGGACAGCCATC 1504
Db 1441 GACACACTTCCCAAGGACATTCACACCAATCTGCTTACAGAAAGGCTGGGACAGCCATC 1500
OY 1505 GAACCAAGTTTCCCACTCAGACCTTGGGGCCAGACCTTCCACCCCTCCCTTGGCGGTA 1564
Db 1501 GAACCAAGTTTCCCACTCAGACCTTGGGGCCAGACCTTCCACCCCTCCCTTGGCGGTA 1560
OY 1565 CCAAGACTCTCTCGGCTCCACCGACCTGTCTTGTCTACACAGCTCTAGACCTGCT 1624
Db 1561 CCAAGACTCTCTCGGCTCCACCGACCTGTCTTGTCTACACAGCTCTAGACCTGCT 1620
OY 1625 GTCTGTCTCTGAGAGCCCGGCGCTGACATCTGTGACATGCTTACCTGTAGAGTCTT 1684
Db 1621 GTCTGTCTCTGAGAGCCCGGCGCTGACATCTGTGACATGCTTACCTGTAGAGTCTT 1680
OY 1685 TCCGTTCTTACCCCAATTAAGTCTTAATGATCAAAAAA 1732

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Db 1681 TCCGTTCTTACCCCAATTAAGTCTTAATGATCAAAAAA 1728

RESULT 4
AAV84191
ID AAV84191 standard; cDNA to mRNA; 1650 BP.
XX
AC AAV84191;
XX
DT 29-MAR-1999 (first entry)
XX
DE Sodium channel receptor hSINAC1 splice variant.
XX
KM hSINAC1; sodium channel receptor; human; algesia; analgesia;
XX ds; cyclic; circular.
XX
OS Homo sapiens.
XX
PN W09854316-1.
XX
PD 03-DEC-1998.
XX
PF 15-MAY-1998; 98WO-EP02884.
XX
PR 30-MAY-1997; 97EP-0401196.
XX
PA (SYNO ) SYNTHELABO.
PI
PR
PI
XX
XX
DR WPI: 1999-070215/06.
DR P-PSDB: AAM88252.
XX
XX
PT A new sodium channel receptor - useful for, e.g. treatment of
PT neuronal degenerative problems, Alzheimer's, Parkinson's disease and
PT morphine dependence
XX
PS Claim 26; Page 43-46; 63pp; English.
XX
XX
CC This is the coding region of a polynucleotide encoding a splice
CC variant (see AAM88252) of a new human sodium channel receptor (see
CC AAM88250), termed hSINAC1. The polynucleotide was obtained from
CC dorsal root ganglia cDNA by PCR amplification using primers (see
CC V84120-21) based on the hSINAC1 polynucleotide (see AAV84189).
CC hSINAC1 is a member of a new class of sodium channel proteins that
CC may be responsible for some nervous system transmissions, or may be
CC used as a target to regulate some transmissions linked to various
CC pathologies. The splice variant cDNA has a 79-nucleotide insert in
CC the 3' portion of the coding region. This alters the reading
CC frame. As dorsal root ganglia are involved in pain perception, the
CC splice variant protein is expected to have a function linked to
CC algesia or analgesia.
XX
SQ Sequence 1650 BP; 298 A; 575 C; 473 G; 304 T; 0 other;

Query Match 91.7%; Score 1588.8; DB 20; Length 1650;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1623; Conservative 0; Mismatches 7; Indels 20; Gaps 1;

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Dp	181	GCTGAGAGGTGGCGCTACTACAGGAGGTGCACACCAAGACTCGCCGTGATGAGGAGAA	244
Oy	282	AGCCACCGGGCTGCTCTTCCGGGCTGTACACCTGTGCACAATCAACCACTGCGCGGCTG	321
Dp	241	AGCCACCGGGCTATCTTCTCCGGGCTGTACACCTGTGCACAATCAACCACTGCGCGGCTG	300
Oy	342	CGCCCTAACGGCCCAAGACCTCACTGGGGGTGGGGTCTGCTGCTGGGGCCGTGGATCCCGCA	381
Dp	301	CGCCCTAACGGCCCAAGACCTCACTGGGGGTGGGGTCTGCTGCTGGGGCCGTGGATCCCGCA	360
Oy	382	GAGCAGCGCGGCTTCTGCGCGGCCCTGGCGGGGCCCTTGACACGCGCGGCTTCATGGCC	441
Dp	361	GAGCAGCGCGGCTTCTGCGCGGGCCCTGGCGGGGCCCTTGACACGCGCGGCTTCATGGCC	420
Oy	442	AGTCCACACTTTGACATGTCGGCAACTATATGCCGTGTGGGCACTCCTGTGATGCATG	501
Dp	421	AGTCCACACTTTGACATGTCGGCAACTATATGCCGTGTGGGCACTCCTGTGATGCATG	480
Oy	502	CTGCTGGACTGTGCCTTCCGGGGCAACCTTGTGGGGCTGAGAACTTCAACACAGATCTTC	561
Dp	481	CTGCTGGACTGTGCCTTCCGGGGCAACCTTGTGGGGCTGAGAACTTCAACACAGATCTTC	540
Oy	562	ACCCGGATGGGAAAGTGCTACATTTAACTGTGGCGCTGATGGGGCAGAGCTGTACAC	621
Dp	541	ACCCGGATGGGAAAGTGCTACATTTAACTGTGGCGCTGATGGGGCAGAGCTGTACAC	600
Oy	622	ACTACTAGGGGTGGCATGTGGGCAATATGGGCTGGACATCATGCTGGACGTGCACAGAGGAA	681
Dp	601	ACTACTAGGGGTGGCATGTGGGCAATATGGGCTGGACATCATGCTGGACGTGCACAGAGGAA	660
Oy	682	TATCTACTGTGTGGAGGGACAATAGAGAGAACCCCGTTTGAAGTGGGGATTCACAGTCA	741
Dp	661	TATCTACTGTGTGGAGGGACAATAGAGAGAACCCCGTTTGAAGTGGGGATTCAGAGTCA	720
Oy	742	ATCCACAGCCAGAGAGAGACCGGCCATCATGATCACTGCTGGGCTTGGGGGTGTCCCGGGC	801
Dp	721	ATCCACAGCCAGAGAGAGACCGGCCATCATGATCACTGCTGGGCTTGGGGGTGTCCCGGGC	780
Oy	802	TACCAAGACTTTGTTTCTTGTGCACAGCAGCAGCTGAGCTTCTGCAACCGCCCTGGGCG	861
Dp	781	TACCAAGACTTTGTTTCTTGTGCACAGCAGCAGCTGAGCTTCTGCAACCGCCCTGGGCG	840
Oy	862	GATTGCACTTACGATCTCGTAACCCCACTATAGAGCAGAGGCCCTGATCCCTGAGGC	921
Dp	841	GATTGCACTTACGATCTCGTAACCCCACTATAGAGCAGAGGCCCTGATCCCTGAGGC	900
Oy	922	TCCCCAGCCCCACAGCCCCAGGCCCTCCCTATACCTTATGGGGTGTGAGCTGGGCTTCGAA	981
Dp	901	TCCCCAGCCCCACAGCCCCAGGCCCTCCCTATACCTTATGGGGTGTGAGCTGGGCTTCGAA	960
Oy	982	ACCCGCTACGTGGCTCGGAAGTGGCGGCTGCCGAATGGTGTATATGCGCAGCGAGCTGCCA	1041
Dp	961	ACCCGCTACGTGGCTCGGAAGTGGCGGCTGCCGAATGGTGTATATGCGCAGCGAGCTGCCA	1020
Oy	1042	GTTGGCAGCCCCCAGAGCTACAGTAACATCTGTGCCACCCCGGCCATTAATGCCATCTTCCG	1101
Dp	1021	GTTGGCAGCCCCCAGAGCTACAGTAACATCTGTGCCACCCCGGCCATTAATGCCATCTTCCG	1080
Oy	1102	AAGAGACTGTGCGGCTGCCCAACCCGTGGCGCAGACAGGGGCTATAGCCCAAGAGGCTCTGC	1161
Dp	1081	AAGAGACTGTGCGGCTGCCCAACCCGTGGCGCAGACAGGGGCTATAGCCCAAGAGGCTCTGC	1144
Oy	1162	ATGGTGGGGAATCCCGAGCCGCGCGCCGCGGCTTCTGTGGCCCGGAAAGCTCAACGCGAGC	1221
Dp	1141	ATGGTGGGGAATCCCGAGCCGCGCGCCGCGGCTTCTGTGGCCCGGAAAGCTCAACGCGAGC	1200
Oy	1222	GAGGCTTACATCCGCGGAAGACTGTGGGCTTGGAGCATCTTCTTTGAGGCGCTCAATAT	1281
Dp	1201	GAGGCTTACATCCGCGGAAGACTGTGGGCTTGGAGCATCTTCTTTGAGGCGCTCAATAT	1260
Oy	1282	GAGACCGTGGGACGAGGAAGGCTATAGATATCAGACTCTGTTGGTATCAATTGGGGG	1344
Dp	1261	GAGACCGTGGGACGAGGAAGGCTATAGATATCAGACTCTGTTGGTATCAATTGGGGG	1320

Oy	1342	CAGATGGGCGCCCTTTCATCTGGGGGACACGCTGCATCTCTGAGATCTCTAGACTACCTC	1401
Oy	1342	CAGATGGGCGCCCTTTCATCTGGGGGACACGCTGCATCTCTGAGATCTCTAGACTACCTC	1401
Db	1321	CAGATGGGGGCTGTTCATCTGGGGGACACTGCTCTACCATCTCTGGAATCTCTAGACTACCTC	1380
Oy	1402	TGTGAGCTGTTCCGAGACAAAGTCTCTGGGATATTTCTGGAACCGACAGACTCCCAAGG	1461
Db	1381	TGTGAGCTGTTCCGAGACAAAGTCTCTGGGATATTTCTGGAACCGACAGACTCCCAAGG	1440
Oy	1462	CACATCCAGCACCAATCTGCTTCAGAAAGGCTGGGAGAGCATCTGAAACCAAGTTCCCCAC	1521
Db	1441	CACATCCAGCACCAATCTGCTTCAGAAAGGCTGGGAGAGCATCTGAAACCAAGTTCCCCAC	1500
Oy	1522	CTCAGCCTGGGCCCC-----AGACTCCACCCCTCCCTGTGGCG	1561
Db	1501	CTCAGCCTGGGCCCCCAGCACTCTGCTGTCTCCGAAGACCTCCACCCCTCCCTGTGGCG	1560
Oy	1562	TCACCAAGAGCTCTCTCCGACCTCCACACGAGACGTGCTACTTTCACACAGCTTAGACT	1621
Db	1561	TCACCAAGAGCTCTCTCCGACCTCCACACGAGACGTGCTACTTTCACACAGCTTAGACT	1620
Oy	1622	GCCTCTGTGTCCCTCGGAGGCCGCCCTTA	1651
Db	1621	GCCTCTGTGTCTCTCGGAGGCCGCCCTTA	1650

RESULT	5
ID	AAV84189
AC	AAV84189 standard; cDNA to mRNA; 1723 BP.
XX	
DT	29-MAR-1999 (first entry)
DE	Sodium channel receptor hSLNAC1 cDNA.
XX	
KW	hSLNAC1; sodium channel receptor; human; neurodegeneration;
KW	Alzheimer's disease; Parkinson's disease; morphine dependence;
KW	chorea; muscular spasm; epilepsy; stroke; cardiac disease;
KW	schizophrenia; depression; nicotine dependence;
KW	amyotrophic lateral sclerosis; multiple sclerosis; inflammation;
KW	pain; cancer; obesity; neurotransmitter; analgesic; anaesthesia;
KW	ds. cyclic; circular.
OS	Homo sapiens.
XX	
FH	Key
FT	Location/Qualifiers
FT	CDS
FT	13..1644
FT	/**tag= a
XX	
XX	W03854316-A1.
XX	
PD	03-DEC-1998.
XX	
PF	15-MAY-1998; 98MO-EP02884.
XX	
PR	30-MAY-1997; 97EP-0401196.
PA	(SYNO) SYNTHELABO.
XX	
PI	Besnard F, Graham D, Renard S;
DR	WPI: 1999-070215/06.
DR	P-PsDB: AAW88250.
XX	
PT	A new sodium channel receptor - useful for, e.g. treatment of
PT	neuronal degenerate problems, Alzheimer's, Parkinson's disease and
PT	morphine dependence
PS	Claim 3; Page 31-34; 63pp; English.
CC	This cDNA clone, designated p3SLNAC1, codes for a new human sodium
CC	channel receptor (see AAW88250) termed hSLNAC1. This is a member of

CC a new class of sodium channel proteins that may be responsible for
CC some nervous system transmissions, or may be used as a target to
CC regulate some transmissions linked to various pathologies.
CC p35NAC1 (ATCC 9797) was isolated from a human cerebellum cDNA
CC library following an expressed sequence tag database screening.
CC Methods for producing hSNAC1 polypeptides by recombinant methods
CC are disclosed. Host cells expressing hSNAC1 can be used to screen
CC for agonists or antagonists of hSNAC1. Such compounds can be used
CC to treat neurodegeneration, hyperalgesia, Alzheimer's disease,
CC Parkinson's disease, chorea, muscular spasm, epilepsy, stroke,
CC cardiac diseases, schizophrenia, depression, nicotine dependence,
CC morphine dependence, amyotrophic lateral sclerosis, multiple
CC sclerosis, inflammation, pain, cancer and obesity, to mimic or
CC antagonise the effects of endogenous transmitter peptides,
CC opioids or anti-opioids, to alter gustative perception, to cause
CC analgesia or anaesthesia, or to diagnose or treat any disorder
CC related to abnormal expression of hSNAC1.

XX Sequence 1723 BP; 331 A; 586 C; 483 G; 323 T; 0 other;

Query Match 91.4%; Score 1583.8; DB 20; Length 1723;
Best Local Similarity 96.2%; Pred. No. 0;
Matches 1657; Conservative 0; Mismatches 7; Indels 59; Gaps 1;

QY 10 GGGGTTCTGGCCATGAGAGCCACCTGAGGCCAGAGAGCCCGGGGAGCCCTTGGGAC 69
DB 1 GGGGTTCTGGCCATGAGAGCCACCTGAGGCCAGAGAGCCCGGGGAGCCCTTGGGAC 60
QY 70 ATCCGCGTTTGGCCAGCACTGCTGATGACAGCGGCTGGGACGCTTTCGGGCGAGCC 129
DB 61 ATCCGCGTTTGGCCAGCACTGCTGATGACAGCGGCTGGGACGCTTTCGGGCGAGCC 120
QY 130 AGCTGAGCCTGCGCGGGGATGTCGAGCGGCGGCTGCTGCTGATGAGTGGCACCCTTC 189
DB 121 AGCTGAGCCTGCGCGGGGATGTCGAGCGGCGGCTGCTGCTGATGAGTGGCACCCTTC 180
QY 190 CTCTACAGAGTGGCTGAGAGGGGCTGCTACTACAGGAGTTCACACAGACTGGCCCTG 249
DB 181 CTCTACAGAGTGGCTGAGAGGGGCTGCTACTACAGGAGTTCACACAGACTGGCCCTG 240
QY 250 GATGAGCGAGAAAGCCAGCGGCTGCTTCCCGGCTGTCACCCCTGTCACATCAACCCCA 309
DB 241 GATGAGCGAGAAAGCCAGCGGCTGCTTCCCGGCTGTCACCCCTGTCACATCAACCCCA 300
QY 310 CTGCGCGCTGCGGCTTAACGCCCAAGCAGCTGAGCTGGGCTGCTGCTGCTGCTGCTG 369
DB 301 CTGCGCGCTGCGGCTTAACGCCCAAGCAGCTGAGCTGGGCTGCTGCTGCTGCTGCTG 360
QY 370 CTGAGATCCCGCAGAGACCGCGCTTCTGCGCGGCCCTGGGCGGCCCTGACCGGCC 429
DB 361 CTGAGATCCCGCAGAGACCGCGCTTCTGCGCGGCCCTGGGCGGCCCTGACCGGCC 420
QY 430 GGGTTCATGCCAGTCCACCTTTGACATGGCGCAACTATGACCCGCTGGGCACTCC 489
DB 421 GGGTTCATGCCAGTCCACCTTTGACATGGCGCAACTATGACCCGCTGGGCACTCC 480
QY 490 CTGAGATGATGCTGCTGAGACTGCTGCTGCGGCCAAGCTTGTGGGCTGAGAACTTC 549
DB 481 CTGAGATGATGCTGCTGAGACTGCTGCTGCGGCCAAGCTTGTGGGCTGAGAACTTC 540
QY 550 ACCAGATCTTCCACCGGATGGGAAAGTGTATACATTTTAACCTGGCGTGTATGGGCA 609
DB 541 ACCAGATCTTCCACCGGATGGGAAAGTGTATACATTTTAACCTGGCGTGTATGGGCA 600
QY 610 GAGCTGCTACCACTAGGGGTGGCATGGGCAATGGGCTGGAGCATGCTGAGAGCTG 669
DB 601 GAGCTGCTACCACTAGGGGTGGCATGGGCAATGGGCTGGAGCATGCTGAGAGCTG 660
QY 670 CAGCAGAGAGAAATATCTACTGCTGAGAGGAGAAATGAGAGAGACCCCGTTTGAAGTGGG 729
DB 661 CAGCAGAGAGAAATATCTACTGCTGAGAGGAGAAATGAGAGAGACCCCGTTTGAAGTGGG 720
QY 730 ATCCGAGTGCAGATCCACAGCCAGAGAGCCGCCATCATGATGAGTGGGCTGGG 789

DB 721 ATCCGAGTGCAGATCCACAGCCAGAGAGACCGCCCATATGATGATGAGTGGGCTGGG 780
QY 790 GTGTCCCGGGGCTACCAAGACCTTTGTTCTTGGCAGCAGCAGCAGCTGAGCTTCTGCCA 849
DB 781 GTGTCCCGGGGCTACCAAGACCTTTGTTCTTGGCAGCAGCAGCAGCTGAGCTTCTGCCA 840
QY 850 CCGCCCTGGGCGATTTGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 909
DB 841 CCGCCCTGGGCGATTTGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 900
QY 910 GATCCCTTGGGCTGGGCGATTTGCAATGATGATGATGATGATGATGATGATGATGATG 969
DB 901 GATCCCTTGGGCTGGGCGATTTGCAATGATGATGATGATGATGATGATGATGATGATG 960
QY 970 CTGCGCTGGGAAACCCGCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1029
DB 961 CTGCGCTGGGAAACCCGCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
QY 1030 GCGGAGCTGCGAGTGTGACAGCCCGCAGCAGTACAGACTGTGCTCCACCGGCTATGAT 1089
DB 1021 GCGGAGCTGCGAGTGTGACAGCCCGCAGCAGTACAGACTGTGCTCCACCGGCTATGAT 1080
QY 1090 GCCATCCTTGGGAAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1149
DB 1081 GCCATCCTTGGGAAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
QY 1150 AAGGAGCTCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1209
DB 1141 AAGGAGCTCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
QY 1210 CTCAACCGCAGCAGCGCTTACATGCGGAGAGACGTGCTGGCTTGGACATCTTCTTGG 1269
DB 1201 CTCAACCGCAGCAGCGCTTACATGCGGAGAGACGTGCTGGCTTGGACATCTTCTTGG 1260
QY 1270 GCCCTCAACTATGAGACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1329
DB 1261 GCCCTCAACTATGAGACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
QY 1330 GACATTTGGGGGCGCAGATGGGCTTTTATGCGGGGCGCAGCTGCTACCATCTGAGATC 1389
DB 1321 GACATTTGGGGGCGCAGATGGGCTTTTATGCGGGGCGCAGCTGCTACCATCTGAGATC 1380
QY 1390 CTGAGACTACTCTGTGAGGTGTTCCGAGACAAAGTCTGGGATATTTTCGAAACCGAAG 1449
DB 1381 CTGAGACTACTCTGTGAGGTGTTCCGAGACAAAGTCTGGGATATTTTCGAAACCGAAG 1440
QY 1450 CACTCCCAAGGCACTTCAGACCAACATCTGCTTCAAGAAAGGCTGGGACAGCATCAAC 1509
DB 1441 CACTCCCAAGGCACTTCAGACCAACATCTGCTTCAAGAAAGGCTGGGACAGCATCAAC 1469
QY 1510 CAAATTTCCCACTCAGGCTGGGCGCCAGACCTTCCACCCCTGCTGCTGCTGCTGCTG 1569
DB 1470 -----GACCTCCCAACCCCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1501
QY 1570 ACTCTCTCGGCTTCCACCGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1629
DB 1502 ACTCTCTCGGCTTCCACCGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1621
QY 1630 TGTCTCTGAGAGCCCGGCTGACATCTGAGACATGCTGAGACATGCTGAGCTGCTTTC 1689
DB 1562 TGTCTCTGAGAGCCCGGCTGACATCTGAGACATGCTGAGACATGCTGAGCTGCTTTC 1621
QY 1690 CTTTACCCCAATTAAGTCTTAATGATCAAAAAA 1732
DB 1622 CTTTACCCCAATTAAGTCTTAATGATCAAAAAA 1664
RESULT 6
AAV84190
ID AAV84190 standard; cDNA to mRNA; 1711 BP.
XX
AC AAV84190;

XX 29-MAR-1999 (first entry)
XX DE Sodium channel receptor hSLNAC1 homologous cDNA.
XX KW hSLNAC1: sodium channel receptor; human; ds; cyclic; circular.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 76..1632
XX FT /*tag= a
XX PN MO9854316-A1.
XX PD 03-DEC-1998.
XX PE 15-MAY-1998; 98WO-EP02884.
XX PR 30-MAY-1997; 97EP-0401196.
XX PA (SYNO) SYNTHELABO.
XX PI Besnard F, Graham D, Renard S;
XX DR WPI; 1999-070215/06.
XX DR P-PSDB; AAM88251.
XX PT A new sodium channel receptor - useful for, e.g. treatment of
XX PT neuronal degenerate problems, Alzheimer's, Parkinson's disease and
XX PT morphine dependence
XX PS Claim 22; Page 37-40; 63pp; English.
XX CC This cDNA sequence, derived from human cerebellum, shows homology
XX CC to novel human sodium channel receptor hSLNAC1 polynucleotide (see
XX CC AA084189), and hybridises under conditions useable for amplification
XX CC or for use as a probe or marker. It codes for a 518-amino acid
XX CC polypeptide (see AAM88251). hSLNAC1 (see also AAM88250) is a member of
XX CC a new class of sodium channel proteins that may be responsible for
XX CC some nervous system transmissions, or may be used as a target to
XX CC regulate some transmissions linked to various pathologies.
XX SQ Sequence 1711 BP; 329 A; 578 C; 481 G; 323 T; 0 other:
Query Match 87.1%; Score 1508.2; DB 20; Length 1711;
Best Local Similarity 95.9%; Pred. No. 0;
Matches 1582; Conservative 0; Mismatches 8; Indels 59; Gaps 1;
QY 84 CAGCACTGCTCGATGACAGGGGCTGGGCGACGCTTTCGGGCCAGGACGCTGAGCCTGCG 143
DB 63 CGGACGAGCTCGATGACAGGGGCTGGGCGACGCTTTCGGGCCAGGACGCTGAGCCTGCG 122
QY 144 CCGGGGATGTTGGGAGGCGGCGGCTGCTGTGCACTGGCCACCTCTCTTACAGAGTGGC 203
DB 123 CCGGGGATGTTGGGAGGCGGCGGCTGCTGTGCACTGGCCACCTCTCTTACAGAGTGGC 182
QY 204 TGAGAGGCTGGCTACTACAGGAGTTCCACACAGAGTGGCTGGATGAGCGAGAAG 263
DB 183 TGAGAGGCTGGCTACTACAGGAGTTCCACACAGAGTGGCTGGATGAGCGAGAAG 242
QY 264 CCACGGCTGCTTTCGCGGCTGTCACCTGTGCAACATCAACCCAGTCGCGCGCTGCG 323
DB 243 CCACGGCTGCTTTCGCGGCTGTCACCTGTGCAACATCAACCCAGTCGCGCGCTGCG 302
QY 324 CCTAACGCCCAACGACCTGACACTGGGCTGGGCTGCTGCTGGGCTGGATCCGCGAGA 383
DB 303 CCTAACGCCCAACGACCTGACACTGGGCTGGGCTGCTGCTGGGCTGGATCCGCGAGA 362
QY 384 GCAGCGCGCTTCTCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 443
DB 363 GCAGCGCGCTTCTCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 422

QY 444 TCCACCTTTGACATGCGGCAACTATGCCCCGCTGTGGGCACTCCCTGGATGACATGCT 503
DB 423 TCCACCTTTGACATGCGGCAACTATGCCCCGCTGTGGGCACTCCCTGGATGACATGCT 482
QY 504 GCTGACGCTGCTTCCGCGGCAACTGTTGGGCTGGAGCTTCCACAGATGTTGAC 563
DB 483 GCTGACGCTGCTTCCGCGGCAACTGTTGGGCTGGAGCTTCCACAGATGTTGAC 542
QY 564 CCGGATGGGAAGTCTACACATTTAACTCTGGCCTGATGGGCGAGAGCTGTCACAC 623
DB 543 CCGGATGGGAAGTCTACACATTTAACTCTGGCCTGATGGGCGAGAGCTGTCACAC 602
QY 624 TACTAGGGGTGCGATGGGCAATGGCTGGACATCATGCTGGACGTGACAGAGGAATA 683
DB 603 TACTAGGGGTGCGATGGGCAATGGGCTGGACATCATGCTGGACGTGACAGAGGAATA 662
QY 684 TCTACTGTGTGGAGGCAATGAGAGAGCCGTTTGTAGGTGGGGAATCCGATGTCACAT 743
DB 663 TCTACTGTGTGGAGGCAATGAGAGAGCCGTTTGTAGGTGGGGAATCCGATGTCACAT 722
QY 744 CCACAGCCAGAGAGAGCGGCCCATGATGATGAGCTGGGCTTGGGCTGTCGCCGCGCTA 803
DB 723 CCACAGCCAGAGAGAGCGGCCCATGATGATGAGCTGGGCTTGGGCTGTCGCCGCGCTA 782
QY 804 CCAGACCTTTTCTTTCGACAGCAGCAGCAGCTGAGCTTCTGCGCACCGCCCTGGGCGA 863
DB 783 CCAGACCTTTTCTTTCGACAGCAGCAGCAGCTGAGCTTCTGCGCACCGCCCTGGGCGA 842
QY 864 TTGCAATTCAGATCTGTGAAACCCCACTATGAGCAGACGCCCTGTGATTCCTTGGCTC 923
DB 843 TTGCAATTCAGATCTGTGAAACCCCACTATGAGCAGACGCCCTGTGATTCCTTGGCTC 902
QY 924 CCCCAGCCCAAGCCGACCCCTCCCTATACCTTATGAGGCTGTGCTGCGCTGGCAAC 983
DB 903 CCCCAGCCCAAGCCGACCCCTCCCTATACCTTATGAGGCTGTGCTGCGCTGGCAAC 962
QY 984 CCGTACTGCTGCTGGAAGTGGGCTGCCGAATGCTGATACATGCCAGGCGAGTGGCAGT 1043
DB 963 CCGTACTGCTGCTGGAAGTGGGCTGCCGAATGCTGATACATGCCAGGCGAGTGGCAGT 1022
QY 1044 GTGCAAGCCCAAGCAGTACAAAGAACTGTGCCACCCGCGCATAGTGGCATTCCTGCA 1103
DB 1023 GTGCAAGCCCAAGCAGTACAAAGAACTGTGCCACCCGCGCATAGTGGCATTCCTGCA 1082
QY 1104 GGACCTGTGGCGCTGCCCAACCCGCTGGCCAGCAGCGGCTTACGCGAGAGCTTCCAT 1163
DB 1083 GGACCTGTGGCGCTGCCCAACCCGCTGGCCAGCAGCGGCTTACGCGAGAGCTTCCAT 1142
QY 1164 GGTGCGGATCCCGAGCGCGCGCGCGCTTCTGTGCGCGGAAAGCTCAACCGCAGCGA 1223
DB 1143 GGTGCGGATCCCGAGCGCGCGCGCGCTTCTGTGCGCGGAAAGCTCAACCGCAGCGA 1202
QY 1224 GGCTTACATTCGGGGAAGAGTGTGGGCTGGGACATCTTGTGAGGCGCTCACTATGA 1283
DB 1203 GGCTTACATTCGGGGAAGAGTGTGGGCTGGGACATCTTGTGAGGCGCTCACTATGA 1262
QY 1284 GACCTGTGAGAGCAAGAGAGCTATGAGATGTACAGAGCTGTTGGTGAATTTGGGGCGCA 1343
DB 1263 GACCTGTGAGAGCAAGAGAGCTATGAGATGTACAGAGCTGTTGGTGAATTTGGGGCGCA 1322
QY 1344 GATGGGCTTTTTCATGGGGCGAGCTGTCTACCATCTCTGAGATCTTACATCTCTG 1403
DB 1323 GATGGGCTTTTTCATGGGGCGAGCTGTCTACCATCTCTGAGATCTTACATCTCTG 1382
QY 1404 TGAGGTGTTCCGAGACAGAGTCTGGGGAATTTTGTGGAAGCAGACGATCCCAAGGCA 1463
DB 1383 TGAGGTGTTCCGAGACAGAGTCTGGGGAATTTTGTGGAAGCAGACGATCCCAAGGCA 1442
QY 1464 CTCCAGACCAATCTGCTTACAGAAAGGCTGGGAGCATGAACCAAGTTCCCACT 1523
DB 1443 CTCCAGACCAATCT----- 1457
QY 1524 CAGCTTGGGCGCCAGACCTCCACCCCTCCCTGTGCGGCTACCAAGACTCTTCCGCCCTC 1583

Dh 865 GATCCGACGACTTTGATCCAGAGCCCTGTGATCCCTTGGTTCCCGACAGCCAGACCC 924
Qy 940 AGCCCTCCCTATACCTTATGGGTGTGCTGCTGAGCTGCGAAGACCCGGCTAGTGGCTCGG 999
Dh 925 AGCCCTCTTATAGTTAATAGTTGTGCTGCTGAGCTGTGAGTCTGCTATGTGTGCTGG 984
Qy 1000 AAGTGGGCTCCGAGATGTTATGTCAGGAGCGAGCTGCGAGTGTGAGCCCGCAGAG 1059
Dh 985 AAGTGTGGCTGTGATGATGATGATGCTGGAAGAACTCCAGATGTGAGCCCGCAGAG 1044
Qy 1060 TACAAGAACTGTGCGCCAGCCGCGCATATAGATCCATCTCTCCAGAGACTCGTGGCCCTGC 1119
Dh 1045 TACAAGAACTGTGCGCCAGCCGCTGTGAGCTATGTGCGAAGAACACAGCTGTGTCTGC 1104
Qy 1120 CCCAACCCGCTGCGCAGCAGCAGCTACAGCCAGAGAGCTCTCCATGCTGCGATCCCGAGC 1179
Dh 1105 CCCAACCCGCTGCGCTACACAGCTATGCTCAAGAGAGCTCTCCATGCTGCGATCCCGAGC 1164
Qy 1180 CGCGCCGCGCGGCTTCTGCGCCGGAAGCTCAACCCGAGAGCCCTAGATCGCGAG 1239
Dh 1165 CGCGCTGAGCTGCTGCTGCTGCGCCGGAAGTACAAACCGAGAGTCTTACATTCAGGAG 1224
Qy 1240 AAGCTGCTGCGCTGAGATCTTCTTTAGAGCCCTCAACTATGAGACCTGAGAGAGAG 1299
Dh 1225 AATGTAAGTGTGATGATCTTCTTTAGAGCCCTCAACTATGAGAGCCGCTGGAACAAAG 1284
Qy 1300 AAGGCTATGAGATGTGAGAGCTGCTGCTGATGAGAGAGAGAGAGAGAGAGAGAGAG 1359
Dh 1285 GCGGCTATGAGATGTGAGAGCTGCTGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAG 1344
Qy 1360 GGGGCGAGCTGTGACCACTCTGAGATCTGAGATCTGAGATCTGAGATCTGAGAGAG 1419
Dh 1345 GAGACAAAGCTGTGATACCTGATGAGATCTGAGATCTGAGATCTGAGATCTGAGAGAG 1404
Qy 1420 AAGGCTGAGATGTGAGAGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1479
Dh 1405 AGAGCTGCTGCTGCTGCTGAG 1464
Qy 1480 CTTCAG 1539
Dh 1465 CTTCAG 1524
Qy 1540 CTTCAG 1599
Dh 1525 CTTCAG 1584
Qy 1600 CTTCAG 1617
Dh 1585 CTTCAG 1602

RESULT 8
AAZ61201
ID AAZ61201 standard; cDNA; 1602 BP.
XX
AC AAZ61201;
XX
DT 30-MAY-2000 (first entry)
XX
DE cDNA encoding a rat acid-sensitive cationic channel 3 (rASIC3).
XX
KW Neuronal acid-sensitive cation channel; ASIC; ASIC 3;
KW Proton-gated cation channel; biphasic desensitisation; amiloride;
KW cation transport channel; acid sensor; pH detection; ds.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT 1..1602
FT CDS /*tag- a
FT /product= "acid-sensitive cationic channel 3"
PN W0200008149-A2.

XX 17-FEB-2000.
PD
XX
XX 05-AUG-1999; 99WO-IB01445.
PF
XX 05-AUG-1998; 98US-0095408.
PR
XX
XX
XX (CNRS) CNRS CENT NAT RECH SCI.
PA
XX
PI Waldmann R, Bassilana F, Lazdunski M, De Welle JR;
XX WPI: 2000-195574/17.
DR
DR P-PSDB; AAY69179.
XX
PT Novel human cation transport protein, Acid Sensing Ionic Channel 3 used
PT to identify substances capable of modulating cation transport channel
PT activity -
XX
XX
XX Disclosure; Page 77-79; 84pp; English.
XX
XX The present sequence encodes a rat neuronal acid-sensitive cation
CC channel 3 (ASIC3) protein. The protein is a proton-gated cation
CC channel subunit that has biphasic desensitisation kinetics with both
CC a rapidly inactivating sodium-selective and a sustained component. The
CC channels are sensitive to amiloride. The specification describes ASIC3
CC proteins, which are expressed in the sensory neurons but not in the
CC brain. The cation transport channel proteins can be used in methods to
CC identify substances capable of modulating the activity of cation
CC transport channels. The human ASIC3 protein is also an acid sensor,
CC and might play an important role in the detection of lasting pH changes
CC in humans.
SQ Sequence 1602 BP; 328 A; 498 C; 434 G; 342 T; 0 other;

Query Match 63.3%; Score 1096.4; DB 21; Length 1602;
Best Local Similarity 81.2%; Pred. No. 1.ee-232;
Matches 1282; Conservative 0; Mismatches 293; Indels 3; Gaps 1;

Qy 43 GAGAGAGCCCGGAG 102
Dh 25 GAGAGAGCCGAG 84
Qy 103 GGGCTGGGCGAGCTTTCGCGGAG 162
Dh 85 GGTGTGGGCGAGCTTTCGCGGAG 144
Qy 163 GCGTGGGCTGTGAG 222
Dh 145 GCTGTGGCTGTGAG 204
Qy 223 AGGAGATTCCACACAG 282
Dh 205 GGGAGATTCCACACAG 264
Qy 283 GCTGTACCTGTGCAATATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 342
Dh 265 GCTGTACCTGTGCAATATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 324
Qy 343 CACTGGGCTGTGAG 402
Dh 325 CACTGGGCTGTGAG 384
Qy 403 GCGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 462
Dh 385 GCACTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 444
Qy 463 CACTGTATGCGGCTGTGAG 522
Dh 445 CACTGTATGCGGCTGTGAG 504
Qy 523 GGGCAACCTGTGAG 582
Dh 505 GGGCAACCTGTGAG 564

QY	583	ACATTTAACTCTGAGCGGTGATGGGGGACAGAGCTGCTACACATACATACAGGAGTGGCATGGGG	642
Dp	565	ACCTTCAACTCTGTGTGCCACGGGTGCAGAGCTCTTACCACCTCCAAAGGGTGTCTGTGC	624
QY	643	AATGGGCTGAGACATCATGCTGTGAGCGTGCAGACAGAGGAATATCTACTGTGTGAGGAGAC	702
Dp	625	AACGCACTAGAGATTTATGTCTAGATGTACAGCAAGAGAGATATCTGCCCATCTCGCAAGAGAC	684
QY	703	AATAGAGAGACCCCGTTTGTAGGTGTGGGGATTCGAGTGCACATCTCCACAGCCAGGAGAGCCG	762
Dp	685	ATGGAAAGAGACCCCGTTTGTAGGTGTGGGGATTCGAGTGCACATCTCCACAGCCAGGATATGACC	744
QY	763	CCCATCTTCATCATAGCTGGGGCTTGGGGGGTGTCCCGCGGGCTTACCAGACCTTTGTCTTTCG	822
Dp	745	CTGTGCATTTACCAAGCTGTGGGCTTGTGGGGAGGCCGCCAGGCGATCAGACCTTTGTGTCTGT	804
QY	823	CAGACAGACAGACGCTGAGCTCTCTGCCACCGCCCTGGGGCGATTGCAGTTCCAGATCTCTG	882
Dp	805	CAGCAGAGAGAACTGAAATTTTCTGTGCCACACACCTGTGGGTGACTGTGAATACGCATCTTGG	864
QY	883	AATCCCAACTA --- TGAAGCAGAGACCCCTGTGATCCCTTGAAGTCCGCCAGCCAGCCAGCC	939
Dp	865	GATCCGACACGACTTTGATTCAGAGCCCTCTGATCCCTTGTGGTTTCCCGACAGCCAGACCC	924
QY	940	AGCCCTCCCTATTAACCTTTATGGGGGTGTGCGCTGTGGCTGCGAAACCCCGTTACGTGTGCTGG	999
Dp	925	AGCCCTCCCTATTAAGTTTAATAGGTTGTGCGCTGTGGCTGTGAGATCTGTGATGTGGCTGG	984
QY	1000	AATGGGCGGCTGCGGAATGGGTGTACATGGCCAGAGCGAGAGTGCACATGTGCAGCCGCCACAGAG	1055
Dp	985	AATGTGTGCTGTGCAATGAATGATGCATATGTCTGTGGAAATCTCCCATGTGTGCAGCCCCACAG	1044
QY	1060	TATCAAGAACTGTGTGCCACCCGGGCATATGATATGCATCTTGTGGAAGAGACTGTGCGCTGTGC	1119
Dp	1045	TACAAAGGACTGTGGCGCACCCACCGCTGTGAAGCGATGTCTGTGAAGAGACAGCGTGTCTGCG	1104
QY	1120	CCCAACCCGTGTGGCCAGCACGCGCTACGCCAGAGAGCTCTCATGTGTGCGATCCCGAGC	1179
Dp	1105	CCCAACCCGTGTGGCTACTATACACCTATATGCCAAGAGACTCTCCATGTGTGGGTATCCCGAC	1164
QY	1180	CGGCGCGCGGCGGCTTCCGTGGGCGCGGAAGCTCAACCGAGAGGAGGCTTACATTTGGCGGAG	1233
Dp	1165	CGCGCTGTACGTGTGCTACTGTGGCCCGGAAATPACAAACCGAGCGAGTCTCTACTATTGCGAG	1224
QY	1240	AACGTGTGGCGCCTGTGACATCTTCTTTGAAGGCCCTCACTATGAGACCGTGTGAGCAGAGAG	1299
Dp	1225	AATGTACTGAGTTTGTGATATCTTCTTTGAAGGCCCTCACTATGAAGCGGTGTGACAAAGAG	1284
QY	1300	AAGGCTATAGATGTACAGCTGTCTTGGTGTGACATTTGGGGGCCAGATGGGCTTTTTCATC	1355
Dp	1285	GGCGGCTATGAAGTGTGGAGCTGTGGGAGACATTGGGGGACAGATGTGGGACTCTTTTATT	1344
QY	1360	GGGGCCAGGCGGCTCACCATCTCTGAGATCTGTAGACTACTCTGTGTAGGTGTTCGAGAGC	1419
Dp	1345	GGAGCAAGGCTGTGTACATCTCTTGAGATCTGTGAATCTGTGATCTGTGTAGGTTTTCAGAGAC	1404
QY	1420	AAGGTCTGTGGATATTTTCTGAAACGACAGACACTTCCAAAGGCACTCCAGCAACAATCTG	1479
Dp	1405	AGAATCTCTGGGGTATTTCTGGAACAGAGAGGCGCTCAAAAAGGCGCTGTGCAAACTCTG	1464
QY	1480	CTTGAGGAAGGGCTGGGGCAGCCATTCGAACCAACCAAGTTCCCACTCTGAGCGCTGTGGGGCCAG	1533
Dp	1465	CTTCAGGAAGAGTGAATGTGCATTCGAACCAATGTTTCCCACTCTGAGCTTATAGGGCCAGG	1524
QY	1540	CTTCCCAACCCCTCCCTGTGGCGTACACAGAGACTCTTCCGCTCCGACGCACTGTCTAC	1599
Dp	1525	CTCTCTTACCACTCCCTGTGCTGTACCAAGACACTCTGTGCGTCCGACGCTACGTTTAC	1584
QY	1600	CTTGTACACAGCTCTAG 1617	
Dp	1585	CTGTCTCAAGGGCTCTAG 1602	

CC	XX	PS	Claim 7; Page 100-101; 105pp; English.
CC	XX	PI	The invention relates to a protein complex forming a heteromultimeric
CC	XX	PP	amiloride-and gadolinium-sensitive proton-gated cation channel
CC	XX	PT	(ASIC-2S.2), where the individual components of the heteromultimeric
CC	XX	Pt	channel include the acid sensing ion channel (ASIC)2A and ASIC3 protein
CC	XX	PR	or their variants having 80% sequence identity, the channel being
CC	XX	PS	activated by protons, acids, low pH solutions, the nucleic acids
CC	XX	PP	encoding the subunits, a recombinant bicistronic vector comprising a
CC	XX	PT	nucleic acid encoding at least two individual subunits or variants of
CC	XX	Pt	ASIC-2S.2, a host cell comprising the vector, an antibody raised against
CC	XX	PR	one of the subunits or a domain which is capable of disrupting assembly
CC	XX	PS	of the ion channel and antagonists of the ion channel. The polypeptides
CC	XX	PI	and polynucleotides are useful for diagnosing a disease or a
CC	XX	PP	susceptibility to a disease in a subject related to expression or
CC	XX	PT	activity of the heteromultimeric channel (e.g. by gene therapy using the
CC	XX	Pt	vector). Such diseases include chronic pain, neuropathic pain such as
CC	XX	PR	diabetic-, cancer- and AIDS (acquired immunodeficiency syndrome)-related,
CC	XX	PS	neurodegenerative diseases such as Alzheimer's disease, Parkinson's
CC	XX	PI	disease, Huntington's disease, Creutzfeldt-Jacob disease, and amyotrophic
CC	XX	PP	lateral sclerosis and dementias, including AIDS-related as well as
CC	XX	PT	convulsions, epilepsy, stroke, anxiety and depression. They are also
CC	XX	Pt	useful for treating cardiovascular diseases such as angina, congestive
CC	XX	PR	
CC	XX	PS	
CC	XX	PI	
CC	XX	PP	
CC	XX	PT	
CC	XX	Pt	
CC	XX	PR	
CC	XX	PS	
CC	XX	PI	
CC	XX	PP	
CC	XX	PT	
CC	XX	Pt	
CC	XX	PR	
CC	XX	PS	
CC	XX	PI	
CC	XX	PP	
CC	XX	PT	
CC	XX	Pt	
CC	XX	PR	
CC	XX	PS	
CC	XX	PI	
CC	XX	PP	
CC	XX	PT	
CC	XX	Pt	
CC	XX	PR	
CC	XX	PS	
CC	XX	PI	
CC	XX	PP	
CC	XX	PT	
CC	XX	Pt	
CC	XX	PR	
CC	XX	PS	
CC	XX	PI	
CC	XX	PP	
CC	XX	PT	
CC	XX	Pt	
CC	XX	PR	
CC	XX	PS	
CC	XX	PI	
CC	XX	PP	
CC	XX	PT	
CC	XX	Pt	
CC	XX	PR	
CC	XX	PS	
CC	XX	PI	
CC	XX	PP	
CC	XX	PT	
CC	XX	Pt	
CC	XX	PR	
CC	XX	PS	
CC	XX	PI	
CC	XX	PP	
CC	XX	PT	
CC	XX	Pt	
CC	XX	PR	
CC	XX	PS	
CC	XX	PI	
CC	XX	PP	
CC	XX	PT	
CC	XX	Pt	
CC	XX	PR	
CC	XX	PS	
CC	XX	PI	
CC	XX	PP	
CC	XX	PT	
CC	XX	Pt	
CC	XX	PR	
CC	XX	PS	
CC	XX	PI	
CC	XX	PP	
CC	XX	PT	
CC	XX	Pt	
CC	XX	PR	
CC	XX	PS	
CC	XX	PI	
CC	XX	PP	
CC	XX	PT	
CC	XX	Pt	
CC	XX	PR	
CC	XX	PS	
CC	XX	PI	
CC	XX	PP	
CC	XX	PT	
CC	XX	Pt	
CC	XX	PR	
CC	XX	PS	
CC	XX	PI	
CC	XX	PP	
CC	XX	PT	
CC	XX	Pt	
CC	XX	PR	
CC	XX	PS	
CC	XX	PI	
CC	XX	PP	
CC	XX	PT	
CC	XX	Pt	
CC	XX	PR	
CC	XX	PS	
CC	XX	PI	
CC	XX	PP	
CC	XX	PT	
CC	XX	Pt	
CC	XX	PR	
CC	XX	PS	
CC	XX	PI	
CC	XX	PP	
CC	XX	PT	
CC	XX	Pt	
CC	XX	PR	
CC	XX	PS	
CC	XX	PI	
CC	XX	PP	
CC	XX	PT	
CC	XX	Pt	
CC	XX	PR	
CC	XX	PS	
CC			

CC heart failure, vasoconstriction, hypertension, atherosclerosis,
 CC renoenositis and bleeding. ASIC-2s.2 plays a role in the regulation of
 CC neurotransmitter release. neuronal excitability or excitotoxicity and is
 CC useful in screening for compounds that regulate neurotransmitter release,
 CC synaptic efficacy, neuroexcitability or neurotoxicity. The present
 CC sequence encodes rat ASIC3A.

XX Sequence 1602 BP; 328 A; 498 C; 434 G; 342 T; 0 other:

Query Match 63.38; Score 1096.4; DB 24; Length 1602;
 Best Local Similarity 81.28; Pred. No. 1,6e-232;
 Matches 1282; Conservative 0; Mismatches 293; Indels 3; Gaps 1;

43 GAGAGGCGCGGCGGAGCCCTCGGACATCCGCGGTTTCGCGAGCAGATGCTGATGAC 102
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 25 GAGCGCCGCGGCGGAGCCCTCGGACATCCGCGGTTTCGCGAGCAGATGCTGATGAC 84
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Oy 103 GGGCTGGGCGGAGCTTCCTGGGCGGAGCAGCTGAGCCCTGGCGCGGGGATGTGGCAGCG 162
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 85 GGTCTGGGCGGAGCTTCCTGGGCGGAGCAGCTGAGCCCTGGCGCGGGGATGTGGCAGCG 144
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Oy 163 GCGCTGGCTCTGAGTGGGCGGAGCAGCTTCCTGACAGTGGCTGAGAGGGTGGCTACTAC 222
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 145 GCTGTGCTCTGTGCTGGGCGGCTTCCTGACAGTGGCTGAGAGGGTGGCTACTAT 204
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Oy 223 AGGAGTTCACCAACAGACTGCGCTGGATGAGGAGAAAGCCACCGGCTGCTCCCG 282
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 205 GGGGAGTTCACCAACAGACTGCGCTGGATGAGGAGAAAGCCACCGGCTGCTCCCG 264
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Oy 283 GCTGTACCTCTGACATACATACCCACTGCGCGCTGGCTTCAGAGCCCAAGAGCCTG 342
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 265 GCTGTGATCTGTATATATACACCCACTGCGCGCTGACCTTCACACCAAGATGCTG 324
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Oy 343 CACTGGGCTGGGCTGCGGCTGCTGGGCTGATCCCGGAGAGACAGCGGCTTCCTGGCG 402
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 325 CACTGGGCTGGGCTGCGGCTGCTGGGCTGATCCCGGAGAGAGCTTCGCTACTTCTG 384
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Oy 403 GCGCTGGGCGGCGGCTGACAGCGCGGCTTCATGCGCACTCCACCTTTGAGATGGCG 462
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 385 GCACTGGGCGGCGGCGGCTGACAGCGCGGCTTCATGCGCACTCCGAGCTTTGAGATGGCA 444
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Oy 463 CAATCTATGCGGCTGCTGGGCTGCTGGGCTGATCCCGGAGAGAGCTTCGCTGCTGCT 522
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 445 CAATCTATGCGGCTGCTGGGCTGCTGGGCTGATCCCGGAGAGAGCTTCGCTGCTGCT 504
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Oy 523 GCGCAACCTGTGGGCTGAGAACTTCAACAGATCTTCACCCGGATGGGAAAGTGTAC 582
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 505 GCGCAACCTGTGGGCTGAGAACTTCAACAGATCTTCACCCGGATGGGAAAGTGTAC 564
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Oy 583 ACATTTAACTGTGGGCTGATGGGCGAGAGCTGCTCACCACTACTAGGGGTGGCATGGGC 642
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 565 ACCTTCAACTGTGGGCTGAGAGAGAGCTGCTCACCACTCAAAAGGGTGGCTGGC 624
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Oy 643 AATGGGCTGGGCTGAG 702
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 625 AAGGAGCTGGGCTGAG 684
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Oy 703 AATGAG 762
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 685 ATGGAAG 744
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Oy 763 CCCATCATCATGAGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 822
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 745 CCGTCCATTTGACAGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 804
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Oy 823 CAG 882
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 805 CAG 864
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Oy 883 AACCCCAACTA--TGAGCCAGAGCCCTGATCCCGTGGGCTGGGCTGGGCTGGGCTGGG 939
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 865 GATCCGACGACTTTGATCCAGAGCCCTGATCCCTTGGGCTGGGCTGGGCTGGGCTGGG 924
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Oy 940 AGCCCTCCCTATTAACCTTATGGGAGTGGCTGGCTGGCTGGAGAACCGGCTAGGCTGG 999
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 925 AGCCCTCCCTATTAACCTTATGGGAGTGGCTGGCTGGCTGGAGAACCGGCTAGGCTGG 984
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Oy 1000 AAGTGGCTCCGAGATGTGTATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1059
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 985 AAGTGGCTCCGAGATGTGTATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1044
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Oy 1060 TACAAG 1119
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1045 TACAAG 1104
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Oy 1120 CCCAACCCGCTGGCAG 1179
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1105 CCCAACCCGCTGGCAG 1164
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Oy 1180 GCGCGCGCGCGCTGCTGGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1239
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1165 GCGCGCTGAGCTGCTGAG 1224
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Oy 1240 AAGCTGGGCGCGGAG 1299
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1225 AATGACTGCTGCTGAGATATCTTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1284
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Oy 1300 AAGGCTATGAGATGTAG 1359
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1285 GCGGCTATGAGATGTAG 1344
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Oy 1360 GGGGCGAGCTGCTGAG 1419
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1345 GAGCAG 1404
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Oy 1420 AAGTCTGAGATATTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1479
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1405 AAGTCTGAGATATTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1464
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Oy 1480 CTTCAG 1539
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1465 CTTCAG 1524
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Oy 1540 CCGCGAG 1599
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1525 CCGCGAG 1584
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Oy 1600 CTTCAG 1617
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1585 CTTCAG 1602
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10

AAAX28161
 ID AAAX28161 standard; cDNA to mRNA; 2962 BP.

XX AAAX28161;

XX 16-JUN-1999 (first entry)

XX Rat Acid sensitive ion channel coding sequence.

XX Acid sensitive ion channel: rat; ASIC; pH mediated pain disorder;

XX Ischemia: gene therapy: proton-gated ion channel: ds.

XX Rattus sp.

XX W09911784-A1.

XX 11-MAR-1999.

XX 28-AUG-1998; 98MO-GB02609.

XX 29-AUG-1997; 97GB-0018365.

XX (UNLO) UNIV COLLEGE LONDON.

XX Akopian AN, Chen C, England S, Wood JN:
 XX WPI: 1999-205188/17.
 DR P-PSDB; AA03186.
 XX
 PT Acid sensitive ion channel (ASIC) proteins - useful in gene therapy
 PT for treatment of pH mediated pain disorders
 XX
 PS Claim 7: Page 43-47; 62pp; English.
 CC This sequence encodes an acid sensitive ion channel (ASIC) of the
 CC invention, isolated from rat dorsal root ganglion. Antisense ASIC DNA or
 CC RNA is useful in gene therapy for downgrading expression of ASIC protein,
 CC for pH mediated pain disorders e.g. in ischemia. The vectors are useful
 CC for incorporating ASIC DNA or RNA for use in gene therapy. Proton-gated
 CC ion channel agonists and antagonists are identified using cells
 CC transfected with ASIC DNA by allowing interaction between the candidate
 CC substance and ASIC protein in the membrane, and measuring interaction
 CC and/or cell response. Partial agonists and antagonists can be identified
 CC by their ability to block the response of the cell to present in a
 CC solution of a given acid pH or any agonist. The hybridisation probes are
 CC useful for screening libraries for ASIC DNA or RNA.
 CC
 SQ Sequence 2962 BP; 655 A; 850 C; 785 G; 672 T; 0 other;
 Query Match 27.3%; Score 472.2; DB 20; Length 2962;
 Best Local Similarity 59.0%; Pred. No. 1e-94;
 Matches 925; Conservative 0; Mismatches 578; Indels 66; Gaps 4;

5 ACACACGCGTTTGGCCATGAGCCACCTCAGGCCAGAGAGCCCGGCGAGCCCT 64
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 251 GGGACTTGGTGGCTTCGCGCAACAGCTGACCTCCATGGTGGCCAGCATGTGTTGTGG 310
 125 CAGGACGCTGAGGCTGCGCGCGGGGAGATGGGCAAGCGCGCTGGCTCTGAGTGCCA 184
 311 AAGGGGGGCCGAGGCGCAAGGAGGCTTATGAGGAGAGGCTTGTATGATGAGTGGTG 370
 185 CTTTCTTACAGAGTGGGCTGAGAGGCTGCTACTAGAGAGAGTTCACACAGCACTG 244
 371 CTTTCTTGGCCAGAGTGGGAGAGGCGTGTCTTATTAACCTACACTACCAAGTACTT 430
 245 CCGTGTATGAGGAG 304
 431 TGTAG 490
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 425 CGCGCGCTTATGAG 484
 596 GCCAG 655
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 656 ACCGGTGGGAG 715
 545 ACTTACACAG 604
 716 ACTTTCAG 775
 605 GGGCAG 664
 776 GGGCGCAG 835

665 ACCTGCAGCAGAGAGAGATATCTACCTGTGTGAGAGCAATGAGAGAGAGAGAGAG 724
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 1559 CCGTCACCA 1567
 1691 CTGCGACCA 1699

RESULT 11
 AAV60842
 ID AAV60842 standard; DNA: 3647 BP.
 AC AAV60842;
 XX
 DT 02-FEB-1999 (first entry)


```
XX Rat acid sensing ionic channel ASIC1B gene.
DE
XX
KM Rat: neuronal cationic channel; amiloride; proton; ASIC; brain; probe;
KM acid sensing ionic channel; hybridisation; primer; PCR; amplification;
KM modulator; acidity; nociception; pain; taste; inflammation; ischaemia;
KM tumour; cerebral neurodegeneration; transgenic animal; knockout animal;
KM gene therapy; Alzheimer's; Parkinson's; Huntington's; disease;
KM amyotrophic lateral sclerosis; cerebellar ataxia; ds.
XX
OS Rattus sp.
XX
XX Key Location/Qualifiers
XX CDS 109..1788
XX FT /*tag= a
XX FT /product= "ASIC1B"
XX FT /note= "acid sensing ionic channel 1B"
XX
XX W09835034-A1.
XX
XX 13-AUG-1998.
XX
XX 11-FEB-1998; 98MO-FR00270.
XX
XX 28-JUL-1997; 97FR-0009587.
XX 11-FEB-1997; 97FR-0001574.
XX
XX (CNRS ) CNRS CENT NAT RECH SCI.
XX
XX Basaglia F, Champigny G, Heurteaux C, Lazdunski M;
XX Waidmann R, Lingueglia E;
XX WPI: 1998-447231/38.
XX P-PSDB: AAM68507.
XX
XX Protein comprising proton-sensitive neuronal channel - useful for
XX screening for analgesics and for treating neurodegeneration
XX
XX Claim 15; Page 34-37; 64pp; French.
XX
XX This sequence represents the gene encoding a rat neuronal cationic
XX channel that is sensitive to amiloride and activated by protons and
XX is designated Acid Sensing Ionic Channel (ASIC). This sequence
XX represents the rat ASIC1B gene. The protein can be used to screen for
XX modulators of these channels, particularly to identify compounds that
XX modulate perception of acidity, as regards nociception (pain) rather than
XX taste. These compounds are used to treat or prevent pain associated with
XX acidity (e.g. in cases of inflammation, ischaemia or some tumours) and as
XX inhibitors of neurodegeneration caused by overexpression of the channels.
XX Antibodies to the protein are used to detect the channels in tissues, and
XX to act therapeutically as channel modulators. The nucleic acid can be
XX used to generate transgenic, particularly knockout, animals for studying
XX ASIC-related disorders, also for gene therapy. The channel protein,
XX or its (ant)agonists, can be used to treat or prevent cerebral
XX neurodegenerative conditions (e.g. Alzheimer's, Parkinson's or
XX Huntington's diseases, amyotrophic lateral sclerosis or cerebellar
XX ataxia.
XX
XX Sequence 3647 BP; 895 A; 853 C; 900 G; 999 T; 0 other:
XX
XX Query Match 27.2%; Score 470.6; DB 19; Length 3647;
XX Best Local Similarity 58.9%; Pred. No. 2.4e-94;
XX Matches 924; Conservative 0; Mismatches 579; Indels 66; Gaps 4;
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Db 350 AAGGGGGCCCAAGGCCAGAGCCCTTATGGGACAGTGGCTTTGTATAGCACTGGGG 409
Qy 185 CCTTCTCTACCAAGTGGCTGAGAGGTGGCTACTACAGGAGTTCACACCAAGACTG 244
Db 410 CTTTCTCTGAGGAGTGGAGGCGCGGTGGCTTATTAACCTGACGATCCACACGACTT 469
Qy 245 CCGTGATGAGGAGAAAGCCACCGGCTGCTCCGCGCTGCAACCTGTGCAACATCA 304
Db 470 TGTAGACGAAGTGGCCACACAGGAGCTGTTCCTCCAGCTCTCACTTGTGCAACACA 529
Qy 305 ACCCACTGGCGCGCTGCGCGCTPAAGCCCAACGACCTGCATGGGCTGGGTGCGTGC 364
Db 530 ATGCGGTGGGTGTTCGCCAGCTACACTACCTGACTTGGCTT---ACGTGGCCCAATGC 586
Qy 365 TGGGGCTGGATCCCGAGAGCAAGCGCGCTTCTCGCGGCCCTGGGGCGGCCCTGCA 424
Db 587 TAGACTGGATGAGATGATGACCCCGGGGTGCC-----CCTTGCTCTCTG 634
Qy 425 CGCCGGCTTCATGCCAGTCCACCTTTGACATGGCGCACTCATGCCCCTGGTGGGC 484
Db 635 GCCCAGAGGCTTTCGCCGGGAGCCCTTTAACTCATGCTTTCTATATGCGCTTGGC 694
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Db 695 ACCGGCTGGAGACATGCTGCTTATTTCTACTGTTGGGGGCCCTGTGCTCCACACA 754
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Db 935 CAGGATCAAAATGAGATCCACAGTCAAGATGAACCCCTTTTATTCAGCACGCTGGCT 994
Qy 785 TGGGGGTGTCGCCGGGCTACACAGACTTGTCTTTCGACAGCAGCAGCAGTGCCTTC 844
Db 995 TTGGTGTGGCTCCAGAGTTCCAGAGCTTTGTCTTTCGACAGAGAGAGAGGCTCATCTAC 1054
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Db 1130 GCGGATTTGATTTGCGAGACGCTTACTGTGTGAGAACTGCAACTGCCGTATGTGACCA 1189
Qy 1025 TGCACGGGAGCTGCGACTGTGACAGCCCCAGCAGTACAAAGAATGTGCCACCGGCCA 1084
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Db 1230 TGGACTTCTTATGTGAGAAAGCAAGCAAGATCTGTGTGTGAGATGCTTGGCAACTGA 1309
Qy 1139 GCGGCTAGCCCAAGAGCTCTTCATGTGCGGATCCCAAGCGCGCCCGCGGCTTCC 1198
Db 1310 CCGGCTAGGAGAGAGCTGTTCATGTGTCAAGATCCCAAGCAAGCTTCGCGCAAGTACC 1369
Qy 1199 TGGCCGGAAGCTCAACGCAAGCGAGGCTCAATGCGGAGAAAGTGTGCGCTTGACA 1258
Db 1258 TGGCCGGAAGCTCAACGCAAGCGAGGCTCAATGCGGAGAAAGTGTGCGCTTGACA 1258
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Db 1370 TGSCAAGAAGTTCACAAATCGAGACATACATAGGAGAGAAATTCGTGTGACA 1429
 QY 1259 TCTTCTTTGAGGCCCTCACTATGAGACCTGGAGCAGAAAGGCTATGAGATGTCAG 1318
 Db 1430 TTTTCTTTGAAATCTTCACATATGAGAACCAATCGAGAGAAAGGCTATGAGATGTCAG 1489
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 Db 1550 TGTGTGAACTCTTGTACTATGCTAGAGGTCAATTAAGCACAGGCTGTGACAGCTGGA 1609
 QY 1439 GGAACGACAGCAGCTCCCAAGGACATCCAGCACCAATCTGCTTCAGAGAAAGGCTGCA 1498
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 QY 1559 CCGTCAACA 1567
 Db 1730 CTGCCAACA 1738
 RESULT 12
 AA61200
 ID AA61200 standard; cDNA, 3647 BP.
 XX
 AC AA61200;
 DT 30-MAY-2000 (first entry)
 XX
 DE cDNA encoding a rat acid-sensitive cationic channel 1B (rASIC1B).
 XX
 KW Neuronal acid-sensitive cation channel; ASIC; ASIC 1B;
 KW proton-gated cation channel; biphasic desensitisation; amiloride;
 KW cation transport channel; acid sensor; pH detection; ds.
 OS Rattus sp.
 FH Key Location/Qualifiers
 FT CDS 109..1788
 FT /tag= "a"
 FT /product= "acid-sensitive cationic channel 1B"
 XX
 PN WO200008149-A2.
 XX
 PD 17-FEB-2000.
 XX
 PF 05-AUG-1999; 99WO-IB01445.
 XX
 PR 05-AUG-1998; 98US-0095408.
 XX
 PA (CNRS) CNRS CENT NAT RECH SCI.
 PI Waldmann R, Bassilana F, Lazdunski M, De Weille JR;
 DR WPI: 2000-195574/17.
 DR P-PSDB; AAY69178.
 XX
 PT Novel human cation transport protein, Acid Sensing Ionic Channel 3 used
 PT to identify substances capable of modulating cation transport channel
 PT activity
 XX
 PS Disclosure: Page 73-76; 84pp: English.
 XX
 CC The present sequence encodes a rat neuronal acid-sensitive cation
 CC channel 1B (ASIC1B) protein. The protein is a proton-gated cation
 CC channel subunit that has biphasic desensitisation kinetics with both
 CC a rapidly inactivating sodium-selective and a sustained component. The

CC channels are sensitive to amiloride. The specification describes ASIC3
 CC proteins, which are expressed in the sensory neurons but not in the
 CC brain. The cation transport channel proteins can be used in methods to
 CC identify substances capable of modulating the activity of cation
 CC transport channels. The human ASIC3 protein is also an acid sensor,
 CC and might play an important role in the detection of lasting pH changes
 CC in humans.
 XX
 SQ Sequence 3647 BP; 895 A; 853 C; 900 G; 999 T; 0 other;
 Query Match 27.2%; Score 470.6; DB 21; Length 3647;
 Best Local Similarity 58.9%; Pred. No. 2.4e-94;
 Matches 924; Conservative 0; Mismatches 579; Indels 66; Gaps 4;
 QY 5 ACGACCGGTTTGGCCATGAGCCCACTGAGGCCAGAGAGGCCCGGCGAGCCCT 64
 Db 230 AAGGAGAAAGAGAAATGAGGACAGGAGCTTGAGATGAGGATGACTACCTA 289
 QY 65 CGGACATCCGCGTGTGGCCAGACATGTCGATGACAGGGGCTGGGCGACGTGTGGGC 124
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 Db 350 AAGGGGCGCCAGGGCCAAAGGACAGGCTTATGGCAGTGGCTTGTATGACTGGGTG 409
 QY 185 CTTTCTCTACCAAGTGGCTGAGAGGGTGGCTACTACAGGAGTTCCACCACCACTG 244
 Db 410 CTTTCTCTGTCAGAGGTAGGGGACCGCGTGTCTATATCTACATCCACAGCTGACTY 469
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 Db 587 TAGGACTGTGATGAGAGTGAAGACCCGCGGTGCG-----CCTTGTCTCTCTG 634
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 Db 875 ACATTCAGCAAGATATGATATTTGCTGTGTGGGAGAGACGAGACATCTCTTGAAG 934
 QY 725 TGGGAGATCCGATGTGATCCACAGCAGAGAGAGGCCCATCATCATGATCAGTGGGCT 784
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 Db 1190 TGCCAGGAGGCGCCCACTACTGCACTCAGAGAGATGAGAGATGATGATCTGCCC 1249
 QY 1085 TAGATGCAATCT-----TGCAAGAGCTCGTGGCTGCCCAACCCGTGGCCAGCA 1138
 Db 1250 TGCACTTCTAGTGAAGAAAGACAGAAATCTGGTGTGTAGATGCTTGCACACTGA 1309
 QY 1139 GCGCTACGCCAGAGAGCTCTGCATGTGGGATCCGAGCCGCGCGCGGCTTCC 1198
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 QY 1199 TGGCCGAGAGCTCAACGCGAGCGCTACATGCGGAGAGAGTGGTGGCCCTGGACA 1258
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 QY 1559 CGGTACCA 1567
 Db 1730 CTGCCACA 1738

RESULT 13
 AAV60840
 ID AAV60840 standard; DNA: 1620 BP.
 XX
 AC AAV60840;
 XX
 DT 02-FEB-1999 (first entry)
 XX
 DE Partial human acid sensing ionic channel gene.
 XX
 KW Human: neuronal cationic channel; amiloride; proton; ASIC; brain; probe;
 KW acid sensing ionic channel; hybridisation; primer; PCR; amplification;
 KW modulator; acidity; nociception; pain; taste; inflammation; ischaemia;
 KW tumour; cerebral neurodegeneration; transgenic animal; knockout animal;
 KW gene therapy; Alzheimer's; Parkinson's; Huntington's; disease;
 KW amyotrophic lateral sclerosis; cerebellar ataxia; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1545
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 FT /product= "partial ASIC"

FT /note= "acid sensing ionic channel; no start codon
 FT is given at the 5' end of the sequence"
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 XX 13-AUG-1998.
 PD 11-FEB-1998; 98WO-FR00270.
 XX 28-JUL-1997; 97FR-0009587.
 PR 11-FEB-1997; 97FR-0001574.
 XX (CNRS) CNRS CENT NAT RECH SCI.
 PA Bassilana F, Champigny G, Heurteaux C, Lazdunski M,
 PI Waldmann R, Lingueglia E,
 DR WPI: 1998-447231/38.
 DR P-PSDB: AAW68505.
 PT Protein comprising proton-sensitive neuronal channel - useful for
 screening for analgesics and for treating neurodegeneration
 PS Claim 13: Page 28-30; 64pp; French.
 XX
 CC This sequence represents a partial gene encoding a human neuronal
 CC cationic channel that is sensitive to amiloride and activated by protons
 CC and is designated Acid Sensing Ionic Channel (ASIC). The protein can be
 CC used to screen for modulators of these channels, particularly to identify
 CC compounds that modulate perception of acidity, as regards nociception
 CC (pain) rather than taste. These compounds are used to treat or prevent
 CC pain associated with acidity (e.g. in cases of inflammation, ischaemia
 CC or some tumours) and as inhibitors of neurodegeneration caused by
 CC overexpression of the channels. Antibodies to the protein are used to
 CC detect the channels in tissues, and to act therapeutically as channel
 CC modulators. The nucleic acid can be used to generate transgenic,
 CC particularly knockout, animals for studying ASIC-related disorders,
 CC also for gene therapy. The channel protein, or its (ant)agonists, can
 CC be used to treat or prevent cerebral neurodegenerative conditions (e.g.
 CC Alzheimer's, Parkinson's or Huntington's diseases, amyotrophic lateral
 CC sclerosis or cerebellar ataxia).
 XX
 SO Sequence 1620 BP; 372 A; 470 C; 465 G; 313 T; 0 other;
 Query Match 26.4%; Score 456.8; DB 19; Length 1620;
 Best Local Similarity 58.5%; Pred. No. 2.2e-91;
 Matches 893; Conservative 0; Mismatches 507; Indels 66; Gaps 3;
 QY 69 CATCCGCTGTTCGCCAGCAACTGCTGATGACAGGGCTGGGCCAGCTTTGGGCCAGG 128
 Db 9 CATCCAGGCTTTGGCCAGCAGCTCCACATGACAGGCGCATGTGCTCTCTACGA 68
 QY 129 CAGCTGAGCTGCGCGCGGGGATGTGGGCAAGCGCCGTGGTCTGTAGTGGCCACTT 188
 Db 69 GCGGCTGTCTGGAAGCGGACATGTGGGCTGTGCTTCTGGGCTGTGGCTGTGCT 128
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 Db 129 GCTGTGTGTGACAGGAGGCTGTGACATCTACTTCCACTACCACTATGCACCACT 188
 QY 249 GGATGAGGAGAAACCCAGCGGCTGCTTCCCGGCTGCAACCTGTGCAACATCAACC 308
 Db 189 CGACAGAGTGGCTGCTTCAAGCTTACCTTCCCTGCTGACGCTGTGCAACATCAAGCA 248
 QY 309 ACTGCGCGCTGCGCGCTTACAGCCCAAGCACTGACATGGGCTGGTGGCTG----- 363
 Db 249 GTTCGCTTTAGCCAAAGTCTCAAGAAATGACCTGTATATCTGGGAGCTGGGCT 308
 QY 364 -----CTGGGCTGTGATCCCGAGAGCAACCGGCTTCTGGCGGCT 407
 Db 309 GCTCAACAAGATGTAGATACAGACACAGATGCAATGAAAGAGCTGTGGAGAT 368
 QY 408 GGGCGGCGCCCTGCAACGCGCGGCTTCAATGCAAGTCCACCTTTGACATGGCGCACT 467

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Db 369 ACTGCAGAGCAAAAGCAACTTCCGAGCTTCAAAOCCAAACCTTACATGCTGATGTT 428
QY 468 CTATGCCCTGCTGGGCACTCCCTGGATGACATGCTGTCGACATGCTCCGCGCA 527
Db 429 CTACACCCGAGCTGGGACAGACATTCGAGCATGCTCTCTCCATCTCCGCGGGA 488
QY 528 ACCTGTGGGCGCTGGAAGTTCACACAGATCTTCAOCCGGATGGGAAATGCTACATTT 587
Db 489 GGTCTGCAGAGCTGAGAACTTCAAGGTGGTCTTCACACCTATGCAAAATGCTACAGTT 548
QY 588 TAACTCTGGCGCTGATGGGGAGAGAGCTCTACACCTATAGGGGGGATGGCAATGG 647
Db 549 CAATCTGGGCGGAATGGGCGGCGCGGCTGAAGACATGAAGGGTGGGACGGGCAATGG 608
QY 648 GTTGACATCATGCTGAGAGCTGACAGCAGAGAGAATATCTACTGTGTGAGGACAAATGA 707
Db 609 GCTGAAATCAATGCTGAGATCCAGCAGACAGATGCTGCTGTGGGGGAGACTGA 668
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QY 768 CATCATCATGCTGGGCTTGGGGGTGTCCCGGGCTACAGACCTTGTCTTCCAGCA 827
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Db 849 GATTTGGATTCTTCGACT-----C 869
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Db 870 CTACAGCATCATGCTGCTGCGATGCTGCTGAGAGCGCTACCTGCTGGAACATGCA 929
QY 1008 CTGCGCAATGCTGATCATCTCCACCGCCCTGGGGCGATTCAGTCTGATGATGAT 1067
Db 930 CTGCGCAATGCTGATCATCTCCAGGGGATGCCCATCTACTCCAGACAGTACAGGA 989
QY 1068 CTGTGGCCCGCCGCGCATGATGCCATCTCTGCGAAGGAC-----TCGNGCGCCGCCC 1121
Db 990 GTGTGAGATCTCTGCTGCTGACTCTCTGCTGAGAGAGGACCAAGATGACTGCTGTGTGA 1049
QY 1122 CAACCGTGGCGCAGCAGCAGCTACGCGCAAGAGCTTCCATGCTGCGATCCCGAGCGG 1181
Db 1050 AATGCTTGCACACCTGACCCGCTATGGCAAGAGCTGTCATGCTCAAGATCCCGAGCA 1109
QY 1182 CGCGCGCGCGCTCTCTGCTGCGCGGAGCTCAACCGCAGCAGGCTTACATCGCGGAGAA 1241
Db 1110 AACTCTGAGCAATGATCTGCGCGGAGGATCAAAATCTGAGCAATGATAGGGAGAA 1169
QY 1242 CGNGCGCGCGCTGAGACATCTTCTTGGAGCGCTCACTATGAGACCGTGGAGAGAGAA 1301
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QY 1422 GGTCTGGGATTTCTTGAAGCAGACATCCCAAAGGATTCAGACATCAATGTGCT 1481
Db 1350 GCTGTGCCAGAGGAAATGCGCAGAGAGGCGCAAAAGAGAGATGCGGAGCAAGGCGG 1409
QY 1482 TCAGAGAGGCTTGGGAGCAGCATGAAACCCAAAGTTCCCACTTACGCTGGGCGCCAGACC 1541

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Db 1410 GGCCTCAGGCTTGGAGAGCTCAAAAGACAAACCCGTGAGAGCTTGGGGCCACCC 1469
QY 1542 TCCCAACCCCTCCCTGTGCGGTACCA 1567
Db 1470 TGGCGGATGACATACGTCGCAACA 1495
RESULT 14
AAZ61198
ID AAZ61198 standard; cDNA; 1620 BP.
AC
XX
AC AAZ61198;
XX
DT 30-MAY-2000 (first entry)
XX
DE cDNA encoding a partial acid-sensitive cationic channel 1A (ASIC1A).
XX
KW Neuronal acid-sensitive cation channel; ASIC; ASIC 1A;
KW proton-gated cation channel; biphasic desensitisation; amiloride;
KW cation transport channel; acid sensor; pH detection; ds.
XX
OS Homo sapiens.
XX
XX
Key Location/Qualifiers
FH 1.1545
FT CDS /tag= a
FT /product= "partial acid-sensitive cationic channel 1A"
FT
XX
XX WO200008149-A2.
XX
PD 17-FEB-2000.
XX
XX 05-AUG-1999; 99WO-IB01445.
XX
XX 05-AUG-1998; 98US-0095408.
XX
XX (CNRS ) CNRS CENT NAT RECH SCI.
XX
XX Waldmann R, Bassilana F, Lazdunski M, De Weille JR;
XX WPI; 2000-195574/17.
XX DR P-PSDB; AAY69176.
XX
XX Novel human cation transport protein, Acid Sensing Ionic Channel 3 used
XX to identify substances capable of modulating cation transport channel
XX activity.
XX
XX Disclosure; Page 67-69; 84pp; English.
XX
XX The present sequence encodes a human partial neuronal acid-sensitive
XX cation channel 1A (ASIC1A) protein. The protein is a proton-gated cation
XX channel subunit that has biphasic desensitisation kinetics with both
XX a rapidly inactivating sodium-selective and a sustained component. The
XX channels are sensitive to amiloride. The specification describes ASIC3
XX proteins, which are expressed in the sensory neurons but not in the
XX brain. The cation transport channel proteins can be used in methods to
XX identify substances capable of modulating the activity of cation
XX transport channels. The human ASIC3 protein is also an acid sensor,
XX and might play an important role in the detection of lasting pH changes
XX in humans.
XX
XX Sequence 1620 BP; 372 A; 470 C; 465 G; 313 T; 0 other;
XX
Query Match 26.4%; Score 456.8; DB 21; Length 1620;
Best Local Similarity 58.5%; Pred. No. 2.2e-91;
Matches 893; Conservative 0; Mismatches 567; Indels 66; Gaps 3;
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Db 69 GCGGCTGCTCTGTAAGCGGGGACTGTGGGCCCCGTGCTTCTGCGGCTGCTGCT 128
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 QY 588 TAACTGTGGGCTGTAGGGGAGAGCTGTGACCACTAAGGAGTGGCATGTG 647
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 Db 609 GCTGGAATCATGCTGGGAGCGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 668
 QY 708 GGAAGACCCCTTTGAGTGGGAGATCCGATGAGATCCACAGCAGAGAGAGAGAGAG 767
 Db 669 CGAGAGCTTTGCAAGAGAGAGATCAAAAGTCAATGATGATGAGTGAACCTCTTT 728
 QY 768 CATGATACGCTGTGGGCTGTGGGCTGTGCTCCGCTACCAACCTTTTGTGCTGCA 827
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 Db 789 GCAGCGGCTCATATACCTGCGCCCACTGTGGGCACTGCAAAAGCTTTTACATGAGCTC 848
 QY 888 CAACATATGAGCAGAGCCCTGTGATCCCTAGGCTCCGCCAGCCCAAGCCCTCC 947
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 QY 948 CTATACCTTATGGGCTGTGCTGCGCTGCGAAACCCGCTACCTGCTCGGAAGTGGG 1007
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 QY 1008 CTGCGAATGTGTATGATGAGCAGAGAGCTGAGTGGAGCCGCCAGCTGCAAGAA 1067
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 Db 990 GTGTGAGATCTGCTGCGCTTCTGTGGTGTGAGAGAGAGAGAGAGAGAGAGAG 1049
 QY 1122 CAACCCGTGCGGAG 1181
 Db 1050 AATGCTTTGCAACCTGAGCCCTATGAGAAAGAGCTGTGCTCAAGATGCCAGCA 1109
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 Db 1110 AGCTTCAAGCAAGTACCTGCGCAAGAGATTCACAAATCTGAGCAATATGAGAGAG 1169

QY 1242 GCTGTGCGCCCTGACATCTTCTTTGAGCCCTCAACTATGAGACCGTGAGAGAGAA 1301
 Db 1170 CATCTGTGTGTGAGCAATTTCTTTGAAGTCTCTCAACTATGAGACCATTAAGAGAGAA 1229
 QY 1302 GGCCTATGATATGTCAGAGCTGTGTGATGATGAGAGAGAGAGAGAGAGAGAGAG 1361
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 QY 1362 GGCAGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1421
 Db 1290 GGCAGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1349
 QY 1422 GGTCTGTGATATTTTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1481
 Db 1350 GCTGTGCGGAG 1409
 QY 1482 TCAG 1541
 Db 1410 GGCCTGTGAG 1469
 QY 1542 TCCACCGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1567
 Db 1470 TGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1495

RESULT 15
 ID AAV60839 standard; DNA: 3562 BP.
 XX AAV60839;
 AC
 AC
 DT 02-FEB-1999 (first entry)
 XX
 DE Rat acid sensing ionic channel ASIC1A gene.
 KW Rat: neuronal cationic channel; amiloride; proton; ASIC; brain; probe;
 KW acid sensing ionic channel; hybridisation; primer; PCR; amplification;
 KW modulator; acidity; nociception; pain; taste; inflammation; ischemia;
 KW tumour; cerebral neurodegeneration; transgenic animal; knockout animal;
 KW gene therapy; Alzheimer's; Parkinson's; Huntington's; disease;
 KW anyotrophic lateral sclerosis; cerebellar ataxia; ds.
 XX
 OS Rattus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 123..1703
 FT /tag= a
 FT /product= "ASIC1A"
 FT /note= "acid sensing ionic channel 1A"
 XX
 XX WO9835034-A1.
 XX PD 13-AUG-1998.
 XX PE 11-FEB-1998; 98WO-FR00270.
 XX PR 28-JUL-1997; 97FR-0009587.
 XX PR 11-FEB-1997; 97FR-0001574.
 XX PA (CNRS) CNRS CENT NAT RECH SCI.
 XX PI Bassilana F, Champigny G, Heurteaux C, Lazdunski M;
 XX PI Waldmann R, Lingueglia E;
 XX DR WPI: 1998-447231/38.
 XX DR P-PSDB; AAW68304.
 PT Protein comprising proton-sensitive neuronal channel - useful for
 PT screening for analgesics and for treating neurodegeneration
 PS Claim 12: Page 24-27; 64pp; French.
 XX

CC This sequence represents the gene encoding a rat neuronal cationic
CC channel that is sensitive to amiloride and activated by protons and
CC is designated Acid Sensing Ionic Channel (ASIC). This sequence
CC represents the rat ASIC1A gene. The sequence was isolated from a rat
CC brain DNA library using a probe amplified by primers AAV60845-V60846.
CC The protein can be used to screen for modulators of these channels,
CC particularly to identify compounds that modulate perception of acidity,
CC as regards nociception (pain) rather than taste. These compounds are
CC used to treat or prevent pain associated with acidity (e.g. in cases of
CC inflammation, ischemia or some tumours) and as inhibitors of
CC neurodegeneration caused by overexpression of the channels. Antibodies
CC to the protein are used to detect the channels in tissues, and to act
CC therapeutically as channel modulators. The nucleic acid can be used to
CC generate transgenic, particularly knockout, animals for studying
CC ASIC-related disorders, also for gene therapy. The channel protein,
CC or its (ant)agonists, can be used to treat or prevent cerebral
CC neurodegenerative conditions (e.g. Alzheimer's, Parkinson's or
CC Huntington's diseases, amyotrophic lateral sclerosis or cerebellar
CC ataxia).

SO Sequence 3562 BP; 905 A; 827 C; 862 G; 968 T; 0 other;

Query Match 26.2%; Score 453.2; DB 19; Length 3562;

Best Local Similarity 58.1%; Pred. No. 1.6e-90;

Matches 902; Conservative 0; Mismatches 578; Indels 72; Gaps 3;

QY 43 GAGAGAGCCCGGGGCGGCGCCCTGGAGATCCGCTGTTCGCCACAGCTGCTGATGCAC 102
DB 147 GAGGTGGGTGGTGTCCGCGCGGTGAGATCCAGGCTTTCGCCACAGCTGCTGATGCAC 206
QY 103 GGGCTGGGACAGCTTCGCGGGGCGAGGAGCTGCGCGGGGGGATGGGAGCG 162
DB 207 GGTCTTCCCACTCTTCTCTCTATGAGCGGCTGTCTGGAAGCGGAGCACTGTGGCCCTG 266
QY 163 GCCGTGCTGTCTGATGAGCGACCTTCCTATCCAGGTGGCTGAGAGGTCGCTACTAC 222
DB 267 TGTCTTCTGGGTTCGCTGCGCGCTCTGCTGTGTGACCTGACGCTGACAGTAC 326
QY 223 AGGAGTTCACCAACCACTGCGCTGATGAGCGAGAAAGCCGCGCTCTTCCG 282
DB 327 TTTCTATATACCAAGTACCAAGCTTGGAGAGTGGCTGCCACAGCTTACCTTCCCT 386
QY 283 GCTGTCACTGTCACATCAACCCAGCTGCGCGCTGCGCCCTAACGCCAACGACTG 342
DB 387 GCTGTCACTGTCACATCAATTCATGAGTTCGCTTTAGCCAGTCTCAAGAAAGACTG 446
QY 343 CACTGGCTGGTCTGCGCTG-----CTGGGCTTGATCCGCA 381
DB 447 TACCATCTGGGAGCTGTGGCCCTGCTCAACAAAGTATGATGCCGAGACACAG 506
QY 382 GAGACGCGCCCTTCTGCGCGGCTGGCGGCCCTGACCGCCGCTTATGCC 441
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QY 562 ACCCGGATGGGAAAGTCTTACATTTAACTCTGGCGCTGATGGGCAAGCTCTCAC 621
DB 687 ACTGGATGGGAGAGTTCATTCACATTCGCGGCAAGATGGCGGCGCCAGCTGAG 746
QY 622 ACTACTAGGGGTGATGGCAATGGGCTGAGATCATGCTGAGCTGACAGAGAGAA 681
DB 747 ACCATGAAGGTGGATGGCATGGCTGAGATCATGCTGAGCTGACAGAGATGA 806
QY 682 TATCTACCTGTGAGAGCAATGAGAGACCCGTTTGAGGTGGGATCCGAGTCA 741
DB 807 TATTGCTGTGAGGAGAGACCGAGACATCTTCGAAGCAGGATCAAGTGCAG 866

QY 742 ATCCACAGCCAGAGAGAGCCGCCATATGATGATGAGTGGGCTTGGGGGTCTCCCGGGC 801
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DB 1182 AAGACAGGAGATCTGT 1241
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QY 1516 CCCCACTGAGCTGGGCGCCCAAGCTTCCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1567
DB 1602 CCTGCGAGAGCTTCCGAGAGATCTGCTGCGGATGAGCTGACCTGCCAACA 1653

Search completed: October 11, 2002, 02:52:12
Job time : 296 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 11, 2002, 02:44:14 : Search time 1943 Seconds
(without alignments)
12051.254 Million cell updates/sec

Title: US-09-530-233-1

Perfect score: 1732
Sequence: 1 tgcacagacgcgtctcgc.....tgcatacaaaaaaaaaa 1732

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: em_esthum:*
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10: gb_estl2:*
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15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	445.6	25.7	452	9	AA884721 am19a09.s
5	439.4	25.4	584	10	BG895217 358498 MA
6	429.2	24.8	498	10	BF344753 602014005
7	415.6	24.0	422	9	A1580095 tk16c11.x
8	401	23.2	429	9	AA449322 zx06e07.s
9	386.8	22.3	469	9	A1684829 wa86b06.x
10	357	20.6	579	9	AM742291 up55b10.y
11	353	20.4	564	9	A1179632 ESR223356
12	342	19.7	342	9	AA448259 zw83e12.s
13	335.2	19.4	1059	10	BG825318 602747771
14	326.8	18.9	503	9	A1024055 ov72c01.s
15	325.6	18.8	835	10	B1548575 603189513
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17	309	17.8	890	9	AL534267 AL534267

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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION DKFZp434B219 r1 434 (synonym: htes3) Homo sapiens cDNA clone
DKFZp434B219 5', mRNA sequence.

ACCESSION AL046680.1 GI:5434743

VERSION
KEYWORDS
SOURCE
ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Poustka, A., Klein, M., Mewes, H.W., Gassenhuber, J. and Wiemann, S.

TITLE EST (Poustka, et al.)

JOURNAL Unpublished (1999)

COMMENT Contact: Poustka A.J.

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Max-Planck-Institute for Molecular Genetics
Innestrasse 73, 14195 Berlin, Germany

Tel: +49-30-84131623
Fax: +49-30-84131128

Email: poustka@mpg-berlin-dahlem.mpg.de

This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;

sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.

No sl sequence available.
This clone (DKFZp434B219) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

location/Qualifiers

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/lab_host="DH10B"
/Note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
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Best Local Similarity 99.5%; Pred. No. 7.9e-99;
Matches 577; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1062 CAAGAACTGTGCCCCACCCGGCATAGATGCCATCTTGGCAAGAGACTGTGGCGCTGCC 1121
Db 1 CAAGAACTGTGCCCCACCCGGCATAGATGCCATCTTGGCAAGAGACTGTGGCGCTGCC 60
OY 1122 CAACCCGTGCGCAGCAGCGCGCTACGCCAAGAGAGCTTCATGGGCGGATCCGAGCG 1181
Db 61 CAACCCGTGCGCAGCAGCGCGCTACGCCAAGAGAGCTTCATGGGCGGATCCGAGCG 120
OY 1182 CGCCGCGCGCGCTTCCTGCGCCGGAGAGCTCAACCGAGCGAGCGCTACATCGCGAGAA 1241
Db 121 CGCCGCGCGCGCTTCCTGCGCCGGAGAGCTCAACCGAGCGAGCGCTACATCGCGAGAA 180
OY 1242 CGTGTGCGCGCTGACATCTTCTTTGAGCGCCCTCAACTATAGACCGTGGAGACAAGAA 1301
Db 181 CGTGTGCGCGCTGACATCTTCTTTGAGCGCCCTCAACTATAGACCGTGGAGACAAGAA 240
OY 1302 GGCCTATAGATATGTCAGAGCTGTGTGTGACATTTGGGGGCCAGATGGGCTTTTCATCG 1361
Db 241 GGCCTATAGATATGTCAGAGCTGTGTGTGACATTTGGGGGCCAGATGGGCTTTTCATCG 300
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Db 361 GGTCTGGATATTTCTGGAACCGAGACACATCCCAAAGGACCTCCAGACCAATCTGCT 420
OY 1482 TCAGAAAGGGCTGGGCGACCATCGAACCAGATTCCCGACCTGAGCGCCCGAGAC 1541
Db 421 TCAGAAAGGGCTGGGCGACCATCGAACCAGATTCCCGACCTGAGCGCCCGAGAC 480
OY 1542 TCCCAACCCCTCTGCTGCGGTACCAAGACTCTCTCGGCTCCACCGCACCTGCTACT 1601
Db 481 TCCCAACCCCTCTGCTGCGGTACCAAGACTCTCTCGGCTCCACCGCACCTGCTACT 540
OY 1602 TGTCAACAGCTAGACCTGCTGCTGCTGCTGAGC 1641
Db 541 TGTCAACAGCTAGACCTGCTGCTGCTGCTGAGC 580

RESULT 2
BM352497/c      594 bp      mRNA      linear      EST 07-JAN-2002
LOCUS      1667e03.x1 HR85 Islet Homo sapiens cDNA 3' similar to TR:09URH4
DEFINITION      Q9URHC ACID SENSING ION CHANNEL 5 SPLICE VARIANT B.; mRNA
sequence.
ACCESSION      BM352497
VERSION      BM352497.1 GI:18084855
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 594)
AUTHORS      Melton,D., Brown,J., Keny,G., Permult,A., Lee,C., Kaestner,K.,
Lemishke,I., Seare,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Maitra,M., Pape,D., Wylie,T., Martin,J., Bilstain,A.,
Schmitt,A., Theising,B., Ritey,E., Ronko,I., Bennett,J., Cardenas
M., Gibbons,M., McCann,R., Cole,R., Tsagarelshvili,R., Williams,T.,
Jackson,Y. and Bowers,Y.
TITLE      Endocrine Pancreas Consortium
JOURNAL      Unpublished (2000)
```

```
COMMENT
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@lhop.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -400p from Glibco
High quality sequence stop: 383.
Location/Qualifiers
1. 594
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="HR85 Islet"
/tissue_type="Purified pancreatic Islet"
/lab_host="DH10B"
/Note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size selected on agarose gel. Average insert size -1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permult Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@im.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
BASE COUNT      116 a      154 c      198 g      126 t
ORIGIN
Query Match      30.3%; Score 524; DB 10; Length 594;
Best Local Similarity 94.5%; Pred. No. 3.6e-89;
Matches 554; Conservative 0; Mismatches 30; Indels 2; Gaps 1;
OY 1140 GCGCTACGCCAAGAGCTCTCCATGTGTGCGGATCCGAGCCG--CGCGCGCGCGCTTC 1197
Db 586 GCGTTCGCCAAGAGAGCTCTCCATGTGTGCGGATCCGAGCGCGCGCGCGCTTC 527
OY 1198 CTGGCGCGGAGGCTCAACCGGAGCGAGCGCTACATCGCGGGAACGTGCTGCGTGGAC 1257
Db 526 CTGGCGCGGAGGCTCAACCGGAGCGAGCGCTACATCGCGGGAAGTGTGCGTGGAC 467
OY 1258 ATCTCTTTGAGGCGCTCAACTATAGAGACGCTGAGAGCAGAGAAGCGCTATAGATGTCA 1317
Db 466 ATTTCTTTGAGGCGCTCAACTATAGAGACCGCTGAGAGCAGAGAAGCGCTATAGATGTCA 407
OY 1318 GAGCTGCTTGTGACATTTGGGGCCAGATGGGCTTTTCATCGGGGCCAGGCTGCTCACC 1377
Db 406 GAGCTGCTTGTGACATTTGGGGCCAGATGGGCTTTTCATCGGGGCCAGGCTGCTCACC 347
OY 1378 ATTCCTGAGATCTAGACTACTCTCTGTGAGGTGTTCGAGACAGAGTCTGGGATATTTC 1457
Db 346 ATTCCTGAGATCTAGACTACTCTCTGTGAGGTGTTCGAGACAGAGTCTGGGATATTTC 287
OY 1438 TGAACGAGACAGCACTCCCAAGGACACTCCAGACCAATCTGCTTCAAGAGGCGTGGG 1497
Db 286 TGAACGAGACAGCACTCCCAAGGACACTCCAGACCAATCTGCTTCAAGAGGCGTGGGA 227
OY 1498 AGCCATGACCAACCAAGTTCGCCACCTCAGCGCTGGGCCCGAGACCTCCACCCCTCCGT 1557
Db 226 AAAATATGAAACCAAGTTCGCCACCTCAGCGCTGGGCCCGAGACCTCCACCCCTCCGT 167
OY 1558 GCGGTACCAAGACTCTCTCGGCTCCACCGGACCGCACTGCTTTCACACACACTAG 1617
Db 166 GCGGTACCAAGACTCTCTCGGCTCCACCGGACCGCACTGCTTTCACACACACTAG 107
OY 1618 ACCTGCTGTCTGCTCTCGGAGCGCGCGCTGACATCTGAGACATGCTAGCCTGACG 1677
Db 106 ACCTGCTGTCTGCTCTCGGAGCGCGCGCTGACATCTGAGACATGCTAGCCTGACG 47
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OY	1678	TAGCTTTCCGTCCTCACCACCAATGAAGTCTATTGCATCAAAA	1723
Dd	46	TAGCTTTCCGTCCTCACCACCAATGAAGTCTATTGCATCAAAA	1
RESULT 3			
LOCUS	AM770119/c		
DEFINITION	AW770119	503 bp	mRNA linear EST 04-MAY-2000
ACCESSION	U83306.x1 Soares_NFL_T_GRC_S1 Homo sapiens cDNA clone IMAGE:2978933	3'	similar to TR:O35240 O35240 PROTON GATED CATION CHANNEL DRASIC ; mRNA sequence.
VERSION	AM770119		
KEYWORDS	AM770119.1 GI:7702158		
SOURCE	EST.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaps-email.nih.gov This clone is available royalty-free through LINL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Seq primer: -400P from Gidco High quality sequence stop: 457.		
FEATURES	location/Qualifiers		
SOURCE	1..503		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:2978933"		
	/clone_id="Soares_NFL_T_GRC_S1"		
	/lab_host="DH10B"		
	/note="Organ: pooled. Vector: pTZ19-D-Pac (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NDHL19W, testis NT1, and B-cell NCI-GARP GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of L.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."		
BASE COUNT	104 a 120 c 170 g 108 t	1 others	
ORIGIN			
Query Match	27.0%;	Score 467;	DB 9; Length 503;
Best Local Similarity	96.6%;	Pred. No. 2.le-78;	
Matches 487;	Conservative 0;	Mismatches 16;	Indels 1; Gaps 1;
OY	1219	AGCGAGGCTACATCGCGAGAACGTGCTGGCCCTGAGACATCTCTTGAGGCCCTCAAC	1278
Dd	503	AGCAAGCGCTACTCGCGGAAAGACGTGCGCCCTGAGACATTTCTTGAGGCCCTCAAC	444
OY	1279	TATGAGACCGTGGACGACAGAAGGCTTATGATGTGAGAGCTGCTGGTGGCATTTGGG	1338
Dd	443	TATGAGACCGTGGACGACAGAAGGCTTATGATGTGAGAGCTGCTGGTGGCATTTGGG	384
OY	1339	GCGCAGATGGGCGCTTTTCATGCGGGGCGAGCCGTCACACATCTGAGAGTCTTAGACTAC	1398
Dd	383	GCGCAGATGGGCGCTTTTCATGCGGGGCGAGCCGTCACACATCTGAGAGTCTTAGACTAC	324
OY	1399	CTCTGTGAGGTGTCGAGACAAGGTCTCTGGATATTTCTTGAAACGACAGCACTCCAA	1458
Dd	323	CTCTGTGAGGTGTCGAGACAAGGTCTCTGGATATTTCTTGAAACGACAGCACTCCAA	264
OY	1458	AGGCACTCGAGACCAATCTGTTAGAGAGGGCTGGGACGCAATCGAACCAGTTCCC	1518

Db	263	AGGCATCTCAGACCAACTCTGTTTGAAGAAGGGCGTAGGACAGCATTCGAACCAACTTCCC	204
OY	1519	CACCTCAGCCTTGCGGCCCCAGACCTCCACACCCTCCCTGTGCGGTACCAAGACTTCTTC	1578
Db	203	CCCCCAGACNTGGGGCCCCAGACCT-CCACCCCTCCCTGTGGCGTCCAGCAAGACTCTTCC	145
OY	1579	GCGTCCACACCGACCTGCTACCTTCTTCACACAGCCTTGACCTGCTGTGTCGTCCTGG	1638
Db	144	GCGTCCACACCGACCTGCTACCTTCTTCACACAGCCTTGACCTGCTGTGTCGTCCTGG	85
OY	1639	AGCCCCGCGCTGACATTCCTTGACATGCTAGCTCAGCTAGCTTTCGCTTCACCCC	1698
Db	84	AGCCCCGCGCTGACATTCCTTGACATGCTAGCTCAGCTAGCTTTCGCTTCACCCC	25
OY	1699	AAATAAAGTCTTAATGATCAAAA	1722
Db	24	AAATAAAGTCTTAATGATCAAAA	1
RESULT 4			
AA884721/c		452 bp	mRNA linear EST 04-JAN-1999
LOCUS			
DEFINITION	aa19a09.s1 Soares_NFL_T_GBC_SI Homo sapiens cDNA clone		
VERSION	IMAGE:1467256.3'		similar to FR:035240 035240 PROTON GATED CATION CHANNEL DRASIC.; mRNA sequence.
KEYWORDS	CHANNEL DRASIC.;		
SOURCE	AA884721..1 GI:2994702		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukariyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
JOURNAL COMMENT	NCI-CGAP http://www.ncbi.nlm.nih.gov/hci/cgap.		
FEATURES	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
Source	Tumor Gene Index		
	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs@email.nih.gov		
	This clone is available royalty-free through LNLN; contact the		
	IMAGE Consortium (info@image.llnl.gov) for further information.		
	Possible reversed clone: similarity on wrong strand		
	Insert Length: 1150 Std Error: 0.00		
	Seq primer: -40m13 fwd. ET from Amersham		
	High quality sequence stop: 134.		
	Location/Qualifiers		
	1. 452		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone_image="IMAGE:1467256"		
	/clone_id="Soares_NFL_T_GBC_SI"		
	/lab_host="DH10B"		
	/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with		
	a modified polylinker; Site_1: Not I; Site_2: Eco RI;		
	Equal amounts of plasmid DNA from three normalized		
	libraries (fetal lung NDHL19W, testis NHT, and B-cell		
	NCI-GAP GCBI) were mixed, and ss circles were made in		
	vivo. Following HAP purification, this DNA was used as		
	tracer in a subtractive hybridization reaction. The driver		
	was PCR-amplified cDNAs from pools of 5,000 clones made		
	from the same 3 libraries. The pools consisted of		
	I.M.A.G.E. clones 297480-302087, 682632-687239,		
	726408-728711, and 729096-731399. Subtraction by Bento		
	Soares and M. Fatima Bonaldo."		
BASE COUNT	92 a 104 c 160 g 96 t		
ORIGIN			
Query Match	25.7%; Score 445.6; DB 9; Length 452;		
Best Local Similarity	99.1%; Pred. NO. 2.3e-74;		
Matches 448; Conservative	0; Mismatches 4; Indels 0; Gaps 0;		
OY	1270	GGCCTCACTATGACACCGTGGAGCAGAAAGCGCTATGACATGTCAGAGCTGCTGGT	1329

Db 452 GCCCTCACTATGAGACCGCTGACAGAGAAGGCCATGAGATCCAGAGCTGCTTGGT 393
 QY 1330 GACATTGGGGGCCAGATGGGCTTTTCATCGGGGGCAGCCGTCACCATCTCTGAGATC 1389
 Db 392 GACATTGGGGGCCAGATGGGCTTTTCATCGGGGGCAGCCGTCACCATCTCTGAGATC 333
 QY 1390 CTAGACTACCTCTGTGAGGTGTTCGAGACAGAGTCTGGGATATTTCTGAAACGACAG 1449
 Db 332 CTAGACTACCTCTGTGAGGTGTTCGAGACAGAGTCTGGGATATTTCTGAAACGACAG 273
 QY 1450 CACTCCCAAGGACACTCCAGACCAATCTGCTTACAGAAAGGCTGGGACCATCGAAC 1509
 Db 272 CACTCCCAAGGACACTCCAGACCAATCTTTCAGAAAGGCTGGGACCATCGAAC 213
 QY 1510 CAAGTTCCCAAGCCTGAGCTGGGGCCAGACCTCCACCCCTGCTGGCTGACCAAG 1569
 Db 212 CAAGTTCCCAAGCCTGAGCTGGGGCCAGACCTCCACCCCTGCTGGCTGACCAAG 153
 QY 1570 ACTCTCTGCGCTTCCACCGCAGCTGCTACCTGTCTACAGAGCTTACAGCTGCTGTCTG 1629
 Db 152 ACTCTCTGCGCTTCCACCGCAGCTGCTACCTGTCTACAGAGCTTACAGCTGCTGTCTG 93
 QY 1630 TGTCCTGGAGCGCCGCGCTGACATCTGACATGCTGCTGCTGCTGCTGCTTCCCT 1689
 Db 92 TGTCCTGGAGCGCCGCGCTGACATCTGACATGCTGCTGCTGCTGCTGCTTCCCT 33
 QY 1690 CTTCACCCCAATTAAGTCTTAATGATCAAA 1721
 Db 32 CTTCACCCCAATTAAGTCTTAATGATCAAA 1

RESULT 5 584 bp mRNA linear EST 05-JUN-2001
 BG895217
 LOCUS 358498 MARC 1Pig Sus scrofa cDNA 5', mRNA sequence.
 DEFINITION BG895217
 ACCESSION BG895217.1 GI:14305458
 VERSION
 KEYWORDS
 EST.
 SOURCE pig.
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 1 (bases 1 to 584)
 Fahnenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
 Stone,R.T., Heaton,M.P., Grose,W.M., Bennett,G.A., Laegreid,W.W.
 and Keele,J.W.
 Design and use of two pooled tissue normalized cDNA libraries for
 EST discovery in swine
 Unpublished (2000)
 CONTACT: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt-trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -mismatch 12 options.
 PCR Primers
 FORWARD: AGGAAGACGCTATGACCAAT
 BACKWARD: GTTTTCCAGTCACGACG
 Plate: 121 row: A column: 15
 Seq primer: ATTTAGCTGACATATAG.
 Location/Qualifiers
 1..584

FEATURES
 source

/organism="Sus scrofa"
 /db_xref="taxon:9623"
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 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
 Library made from pooled tissue from day 11, 13, 15, 20,
 and 30 embryos."

BASE COUNT 104 a 195 c 173 g 112 t
 ORIGIN

Query Match 25.4%; Score 439.4; DB 10; Length 584;
 Best Local Similarity 85.9%; Pred. No. 3, 4e-73;
 Matches 501; Conservative 0; Mismatches 76; Indels 6; Gaps 1;

QY 866 GCAGTTCAGCATCTGTAACCCCACTATGAGCAGAGCCCTGTGATCCCTAGGCTGCC 925
 Db 1 GCAGTTCAGCATCTGTAACCCCACTATGAGCAGAGCCCTGTGATCCCTAGGCTGCC 60
 QY 926 CCAGCCCAAGCCCC-----AGCCCTCCATACCTTATGGGGTTCGCTGGCTGG 979
 Db 61 CCAGTCCCAAGCCCGGTGCCAAGCCCTCCATACCTTATGGGGTTCGCTGGCTGGC 120
 QY 980 AAACCCGCTACGTCGTCGGAATGGGGCTCCGATGGGTGATACATCCAGGAGAGTGC 1039
 Db 121 AGACTGCTTTGTGACTCGGAAGTGGGCTGCGGAATGATGATATGCTGGCGGCGCGC 180
 QY 1040 CAGTGTGACAGCCCAAGCAGTACAGAACTGTGCCACCCGCGCATATGATGCTATC 1099
 Db 181 CAGTGTGACAGCCCAAGCAGTACAGAACTGTGCCACCCGCGCATATGATGCTATC 240
 QY 1100 GCAGGACTGTCGCTGCTGCCCCCAACCCGTGCGCAGACAGCGGCTACGCAAGAGCTCT 1159
 Db 241 GGCAGGAGCGTGTGCTACCTGCCCCCAACCCGTGCGCAGACAGCGGCTACGCAAGAGCTCT 300
 QY 1160 CCATGGTGGGATCCGAGCGCGCGCGGCGGCTTCCGTGGCGGGAAGCTCAACCGCA 1219
 Db 301 CCATGGTGGGATCCGAGCGCGCGCGGCGGCTTCCGTGGCGGGAAGCTCAACCGCA 360
 QY 1220 GCGAGGCTTACATCGCGGAGAAAGTGTGCTGAGCATCTTCTTGAAGCCCTCACT 1279
 Db 361 GCGAGGCTTACATCGCGGAGAAAGTGTGCTGAGCATCTTCTTGAAGCCCTCACT 420
 QY 1280 ATGAGACCTGTGAGCGAGAAAGAGGCTTATGATGTCAAGCTGCTTGTGATTTGGG 1339
 Db 421 ACAGACGCTGTGAGCGAGAAAGAGGCTTATGATGTCAAGCTGCTTGTGATTTGGG 480
 QY 1340 GCCAGTGGGCTTTTCATCGGGGGCCAGCGCTGTCACATCCGATCGATCTAGACTAC 1399
 Db 481 GCCAGTGGGCTTTTCATCGGGGGCCAGCGCTGTCACATCCGATCGATCTAGACTAC 540
 QY 1400 TCTGTGAGGTGTCGAGACAAAGTCTTGGATATTTCTGGAA 1442
 Db 541 TCTGTGAGGTGTCGAGACAAAGTCTTGGATATTTCTGGAA 583

RESULT 6 498 bp mRNA linear EST 22-NOV-2000
 BF344753
 LOCUS 602014005F1 NCI CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4149960
 DEFINITION 5', mRNA sequence.
 ACCESSION BF344753
 VERSION BF344753.1 GI:11292199
 KEYWORDS
 EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 498)
 NIH-MGC http://mgc.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: David N. Louis, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMU at:
 http://image.llnl.gov

REFERENCE 1
 AUTHORS NIH-MGC
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT CONTACT: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: David N. Louis, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMU at:
 http://image.llnl.gov

Plate: LLM9412 row: 1 column: 01
High quality sequence stop: 485.
Location/Qualifiers
1. 498

FEATURES
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/db_xref="taxon:9606"
/clone="IMAGE:4149960"
/clone_1lb="NCI_CGAP_Brn64"
/tissue_type="gliblastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: Brain; Vector: pCMV-Sport6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.57 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 112 a 171 c 114 g 101 t
ORIGIN

Query Match 24.8%; Score 429.2; DB 10; Length 498;
Best Local Similarity 95.2%; Pred. No. 2.8e-71;
Matches 461; Conservative 0; Mismatches 3; Indels 20; Gaps 1;

QY 1269 GGGCCCTCAACTATGAGACCGTGGAGCAGAAAGGCTATGAGATGTGAGAGCTGCTGG 1328
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DB 12 GGGCCCTCAACTATGAGACCGTGGAGCAGAAAGGCTATGAGATGTGAGAGCTGCTGG 71
QY 1329 TGACATTTGGGGGCGACATGGGCTTTTCATCGGGGCGACGCTGTCACCATCTCGAGAT 1388
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DB 72 TGACATTTGGGGGCGACATGGGCTTTTCATCGGGGCGACGCTGTCACCATCTCGAGAT 131
QY 1389 CCTAGACTACTCTGTGAGGTGTTCGAGACAAAGTCTGGGATTTTGTGAAACCGACA 1448
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DB 132 CCTAGACTACTCTGTGAGGTGTTCGAGACAAAGTCTGGGATTTTGTGAAACCGACA 191

QY 1449 GCACTCCCAAGGCACTCCAGACCAATGCTTTCAGGAAGGCTGGGACCATGGAAC 1508
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DB 192 GCACTCCCAAGGCACTCCAGACCAATGCTTTCAGGAAGGCTGGGACCATGGAAC 251

QY 1509 CCNAGTTCCCACTAGCTGAGCTGGGGCC-----AGACCTCCACAC 1548
|||||
DB 252 CCNAGTTCCCACTAGCTGAGCTGGGGCC-----AGACCTCCACAC 311

QY 1549 CCTCCCTGTGGCGTACCAAGACTCTCTCCGCTCCACGCACTGCTACTTGTTCACA 1608
|||||
DB 312 CCTCCCTGTGGCGTACCAAGACTCTCTCCGCTCCACGCACTGCTACTTGTTCACA 371

QY 1609 CAGCTTAACCTGCTGTGTCTGCTGGAGCGCCGCTGACATCTGGAGATGCTTA 1668
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DB 372 CAGCTTAACCTGCTGTGTCTGCTGGAGCGCCGCTGACATCTGGAGATGCTTA 431

QY 1669 GCCTGACGTAGCTTTCCGCTTTCACCCCAATAAGTCTTAATGATCAAAAAA 1728
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DB 432 GCCTGACGTAGCTTTCCGCTTTCACCCCAATAAGTCTTAATGATCAAAAAA 491

QY 1729 AAAA 1732
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DB 492 AAAA 495

RESULT 7
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LOCUS A1580095/c
DEFINITION tk16c11.x1 Soares.NHMPu.S1 Homo sapiens cDNA clone IMAGE:2151188
3' similar to TR:035240 O35240 PROTON GATED CATION CHANNEL DNASIS.
; mRNA sequence.

ACCESSION A1580095
VERSION A1580095.1 GI:4564471
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 422)
AUTHORS NCI-Cgap <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert length: 493 Std Error: 0.00
Seq primer: -40UP from Glibco
POLYA-NO.

FEATURES
source
Location/Qualifiers
1. 422
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2151188"
/clone_1lb="Soares.NHMPu.S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pT7n3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NDHM, pregnant uterus
NBHPU, and fetal heart NBH19W) were mixed, and ss circles
were made in vitro. Following NRP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260332-265233,
340488-345479, and 484488-489479."

BASE COUNT 89 a 97 c 151 g 85 t
ORIGIN

Query Match 24.0%; Score 415.6; DB 9; Length 422;
Best Local Similarity 99.1%; Pred. No. 1e-68;
Matches 418; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1302 GGGCTTNGAGATGTCAGAGCTGCTGTGATTTGGGGGCGAATGGGCTTTTCATCGG 1361
|||||
DB 422 GGGCTTNGAGATGTCAGAGCTGCTGTGATTTGGGGGCGAATGGGCTTTTCATCGG 363

QY 1362 GGGCAGCTGTGCTCACCATCTCGAGATCTAGACTCTGTGAGGTGTTCGAGACAA 1421
|||||
DB 362 GGGCAGCTGTGCTCACCATCTCGAGATCTAGACTCTGTGAGGTGTTCGAGACAA 303

QY 1422 GGTCTGGGATATTTGTGGAACCGACAGACATCCCAAAGGCTCCAGACCAATGTCT 1481
|||||
DB 302 GGTCTGGGATATTTGTGGAACCGACAGACATCCCAAAGGCTCCAGACCAATGTCT 243

QY 1482 TCAGGAAGGGCTGGGAGGCGATGGAACCAAGTTCCCACTGAGCTGGGGCCGAGAC 1541
|||||
DB 242 TCAGGAAGGGCTGGGAGGCGATGGAACCAAGTTCCCACTGAGCTGGGGCCGAGAC 183

QY 1542 TCCACACCTCCCTGTGCGGTACCAAGACTCTCTCGGCTCCACGCACTGCTACCT 1601
|||||
DB 182 TCCACACCTCCCTGTGCGGTACCAAGACTCTCTCGGCTCCACGCACTGCTACCT 123

QY 1602 TGTACACAGCTTAACCTGCTGTGTCTGCTGGAGCGCCGCTGACATCTGGAC 1661
|||||
DB 122 TGTACACAGCTTAACCTGCTGTGTCTGCTGGAGCGCCGCTGACATCTGGAC 63

QY 1662 ATGCTTAGGCTGACGTAGCTTTCCGCTTTCACCCCAATAAGTCTTAATGATCA 1721
|||||
DB 62 ATGCTTAGGCTGACGTAGCTTTCCGCTTTCACCCCAATAAGTCTTAATGATCA 3

QY 1722 AA 1723
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DB 2 AA 1

RESULT 8
AA49322/c 429 bp mRNA linear EST 04-JUN-1997
LOCUS AA49322/c

DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
2x06e07.s1 Scores total fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:785700_3, similar to TR:G1280441 G1280441 DEGENERIN CHANNEL MDG. ;, mRNA sequence.	AA449322	AA449322	AA449322.1	GI:2163171	EST.					
human.										
Homo sapiens										
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.										
1 (bases 1 to 429)										
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Giesels,G., Jost,S., Kucaba,T., Lacey,K., Le,N., Lennon,G., Merri,M., Martin,J., Moore,B., Schabelenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wyllie,T., Waterston,R. and Wilson,R.										
Washu-Weirck EST Project 1997										
Unpublished (1997)										
Contact: Wilson RK										
Washington University School of Medicine										
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108										
Tel: 314 286 1800										
Fax: 314 286 1810										
Email: est@watson.wustl.edu										
This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.										
Possible reversed clone, similarity on wrong strand										
Seq primer: -41m3 fwd. ET from Amersham										
High quality sequence stop: 283.										
Location/Qualifiers										
1..429										
/organism="Homo sapiens"										
/db_xref="GDB:5983318"										
/db_xref="taxon:9606"										
/clone="IMAGE:785700"										
/clone_11b="Scores_total_fetus_Nb2HF8_9w"										
/dev_stage="8-9 weeks"										
/lab_host="DH10B"										
/note="vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from pooled 8-9 week (total) fetus material with a Not I - oligo(dT) primer (5' TGTATCCAACTGTGAAGGGGAGGCGCGCTTAATTTTTTTTTTTT 3'). Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Scores and M. Fatima Bonaldo. "										
BASE COUNT	89 a	100 c	151 g	89 t						
ORIGIN										
Query Match	23.2%	Score 401;	DB 9;	Length 429;						
Best Local Similarity	97.4%;	Pred. No. 6e-66;								
Matches 418;	Conservative 0;	Mismatches 10;	Indels 1;	Gaps 1;						
1294	CAGAGGAGGCGCTATGACATCTCAAGACGCTGCTGGACATTTGGGGCCAGATGGGCGCTT	1353								
1295										
429	CGGAAGAAGCGGTATGAATGTCAAGCGCTGTTGACATTTGGGGCCAGATGGGCGCTT	370								
1354	TTTCATCGGGGGCAGCGCTGCT-CACCATCTCGAGATCTCAGACTACTCTGTGAGGTGTT	1412								
1355										
359	TCGAGCGGGCCAGCGCTGCTGTCGACCATCTCTCGAGATCTCTAGACTACTCTGTGAGGTGTT	310								
1413	CCGAGACAAGTCTCTGGGATATTTCTGGAAACGACGACGACTCTCCAAAGGACATCCAGC	1472								
1414										
309	CCGAGACAAGGTCCTGGGATATTTCTGGAAACGACGACGACTCTCCAAAGGACATCCAGC	250								
1473	CATATTCCTTCAAGAGGGCTGGGACGACCATGAACCAAGTTCCCAACCTTAGCTTGGG	1532								
1474										
249	CAATCTGCTTCGAGGAAGGCTGGGACGACATCAACCCAAAGTTCCCAACCTTAGCTTGGG	190								
1533	CCCGAGACTCCGACCCCTGCGCTGGGGGTACCAAGAACTCTCTCGGCTCCACAGGAC	1592								

QY	1593	CHGCACCTGTGCACAGAGCTGTACACCGCGTGTGTCTCTCGAGAGCCGCCCTGAC	1652
Db	129	CTGCTACCTGTGCACAGAGCTGTACACCGCGTGTGTCTCTCGAGAGCCGCCCTGAC	70
QY	1653	ATTCCTGCACATGCCCTGACAGCTAGCTTTTCGCTTTCACCCCAATAAAGTCTTAA	1712
Db	69	ATTCCTGCACATGCCCTGACAGCTAGCTTTTCGCTTTCACCCCAATAAAGTCTTAA	10
QY	1713	TGCATCAAA 1721	
Db	9	TGCATCAAA 1	
RESULT 9			
LOCUS	AI684829	469 bp	mRNA
DEFINITION	wa6b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone		linear EST 07-MAR-2000
ACCESSION	IMAGE:2303027 3'		similar to TF:075906 075906 PROTON-GATED CATION
VERSION	CHANNEL SUBUNIT.1, mRNA sequence.		
KEYWORDS	AI684829		
ORGANISM	AI684829.1	GI:4896123	
SOURCE	EST.		
REFERENCE	human.		
AUTHORS	Homo sapiens		
TITLE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
JOURNAL	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
COMMENT	1 (bases 1 to 469)		
	NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap .		
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
	Tumor Gene Index		
	Unpublished (1997)		
	Contact: Robert Strusberg, Ph.D.		
	Email: cgapbs-rfemail.nih.gov		
	This clone is available royalty-free through LNL; contact the		
	IMAGE Consortium (info@image.llnl.gov) for further information.		
	Insert Length: 563 Std Error: 0.00		
	Seq primer: -40UP from Gdbco		
	High quality sequence stop: 433.		
FEATURES			
SOURCE			
	location/Qualifiers		
	1..469		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:2303027"		
	/clone_lib="Soares_NFL_T_GBC_S1"		
	/lab_host="DH10B"		
	/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with		
	a modified polylinker; Site.1: Not I; Site.2: Eco RI;		
	Equal amounts of plasmid DNA from three normalized		
	libraries (fetal lung NBHL19W, testis NHT, and B-cell		
	NCI-GCAP-GCBI) were mixed, and ss circles were made in		
	vitro. Following HAP purification, this DNA was used as		
	tracer in a subtractive hybridization reaction. The diver		
	was PCR-amplified cDNAs from pools of 5,000 clones made		
	from the same 3 libraries. The pools consisted of		
	I.M.A.G.E. clones 297480-302087, 682632-687239,		
	726408-728711, and 729096-731399. Subtraction by Bento		
	Soares and M. Fatima Bonaldo.		
BASE COUNT	101 a	107 c	151 g 110 t
ORIGIN			
Query Match	22.3%	Score 386.8;	DB 9; Length 469;
Best Local Similarity	87.5%;	Pred. No. 2.9e-63;	
Matches 460;	Conservative 0;	Mismatches 7;	Indels 59; Gaps 1;
QY	1207	AAGCTCAACCGCAGGAGAGCTACTATCCGCGGAGAACGTGCTGGCCCTGACATCTTCTT	1266
Db	469	AAGCTCAACCGCAGGAGAGCTACTATCCGCGGAGAACGTGCTGGCCCTGACATCTTCTT	410
QY	1267	GAGGCGCTCACTATGAGACCGTGGAGAGAGAAGAGCGCTATGAGATGTCAGAGCTGCTT	1326
Db	409	GAGGCGCTCACTATGAGACCGTGGAGAGAGAAGAGCGCTATGAGATGTCAGAGCTGCTT	350

Oy	1327	GGTGCATTTGGGGGGGCAATGGGAGCCTTTTCAATCGGGGGCAGCCTGTACCAATTCGCGAG	1386
Db	349	GGTGCATTTGGGGGGGCAATGATGGGCTTTTCAATCGGGGGCAGCCTGTACCAATTCGCGAG	290
Oy	1387	ATCCTAGACTACCTCTGTGTAGAGTGTTCGAGACAAGAGTCTTGGGATATTTCTGGAAACGA	1446
Db	289	ATCCTAGACTACCTCTGTGTAGAGTGTTCGAGACAAGAGTCTTGGGATATTTCTGGAAACGA	230
Oy	1447	CAGCACTCCCAAGGACACTCCAGCACCAATCTGCTTACAGGAAGGCGTGGGACCATCGA	1506
Db	229	CAGCACTCCCAAGGACACTCCAGCACCAATTT-----	198
Oy	1507	ACCCAAGTTCCCCACACTCAGCCTGGGGCCCAAGACCTCCACCCCTTCCCTGTGCGCTCACC	1566
Db	197	-----GACCTCCACCCCTTCCCTGTGCGCTCACC	169
Oy	1567	AAGACTCTCTCGCGCTCCACCGACGACACTGCTACCTTTGTACACAGACTGTAGACCTGTGT	1626
Db	168	AAGACTCTTTCCGCTCTCCCGCCCGCACCTGTCTACCTTTGTACACAGACTGTAGACCTGTGT	109
Oy	1627	CTGTGTCTCTGGAGCCCGCCCTGCACATCTGTGGACATGCTTAGCCTGCACGTAGCTTTTC	1686
Db	108	TTGTGTCTCTGGAGCCCGCCCTGCACATCTGTGGACATGCTTAGCCTGCACGTAGCTTTTC	49
Oy	1687	CGTCTTCAACCCCAATATAAGTCTTAATGATCTAATAAAAAAAAAA	1732
Db	48	CGTCTTCAACCCCAATATAAGTCTTAATGATCTAATAAAAAAAAAA	3

RESULT	LOCUS	DEFINITION
10	AW742291	579 bp mRNA linear EST 07-SEP-2000 up55b10.y1 Soares_mouse.MME Mus musculus cDNA clone IMAGE:2779963 5' similar to FR:035240 035240 PROTON GATED CATION CHANNEL DRASIC.

ACCESSION	AW742291	
VERSION	AW742291.1	GI:7654076
KEYWORDS	EST.	
SOURCE	house mouse, "	
ORGANISM	Mus musculus	

REFERENCE
1 (bases 1 to 579)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

Tumor Gene Index
Unpublished (1997)
Other_ESts: up55b10.x1

This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: -40RP from Gldco
High quality sequence stop: 480.

FEATURES	Location/Qualifiers
source	1. .579

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/organism="Mus musculus"
/strain="C3H x 101 (F1 stock)"
/db_xref="taxon:10090"
/clone_image="2779963"
/clone_id="Soares_mouse_NMIE"
/sex="male"
/dev_stage="newborn"
/lab_host="DH10B"
/notes="Organ: inner ear, 170 pooled; Vector: pTTT3D-Pac;
Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed
with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAAGTGGAGCGCGCCGACACTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pTT73 vector. Library
is normalized, and was constructed and donated by Bento
Soares and M. Fatima Bonaldo (University of Iowa) and R.

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BASE COUNT	118 a	184 c	158 g	119 t
ORIGIN	Hardisty, A. Varela-Carver, P. Mburu and S.D.M. Brown (MRC UK Mouse Genome Centre and Mammalian Genetics unit, Harwell, UK). ^a			

Query Match	20.6%	Score 357	DB 9	Length 579
Best Local Similarity	81.0%	Pred. No. 1.2e-57		
Matches 430	Conservative	0	Mismatches 95	Indels 6
				Gaps 1

QY 706 GAGGAGACCCCGTTGAGTGGGGATCCGATCAGATCCACGAGCCAGAGGAGGCCGCC 765

Db 55 GAGGAGACCCCAATTGAGTGGGGATCCGATCAGATCCACGAGCCAGAGGAGAACCCCTT 114

[illegible]

QY 826 CACGACAGCTGAGTTCCTCGCCACCGCCCTGGGGGCATTTGCGATTCAAGCATCTGTGAC 885
 ||| ||||| |
Db 175 CAACGACACTGAGTTTCTTGCCACCACCTCGGGGTGCTGCATACCGCATTGTGGAT 234
 |||||

QY	886	235	Db
CCCAACTGTGAGCCAGAGCCCTGTGATCCCTCTGAGGCTCCGCCAGGCCAGCCCAAGCCCT		CCGACATTGATCCAGAGCCCTCTGATCCCTCTGAGGCTC-----CCCTAGCTCCAGCCCT	945
			288

Oy CCTATTACCTTTATGGGAGTGCACCTGGCCTGGGAACCCCGTAGCTGTGACTCGAAGTCG
946 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT
D8 CATTATACCTTAATAGGAGTGTCGCCCTGGCCTGTAGTATACGCACTAATGTGTGGCTCGGAATGCC
289

0y 1006 GGCTGCCCAATGGTGTACATGCCAGGCGACGTCGCATGTGTGACGCCCCAGCAGTACAG 1065
 |||||
 349 GGATGTGCAATGTGCATATGCTTGGAACTCCCCAGTGTGACGCCCCAGCAGTACAG 408
 |||||

Db 409 GACTGTGCCAGCCACGCTCTGACGCTATGCTCGGAAGAAGACACTTGTGTCTCTCCCAAC 468

Db 469 CCGTGGCCACTACACGCTATGCGCAGAAGAGACTTCCATGTGTGGGATTCGCCACCGCGCT 528

Db	529	7CAGCTGCTACCTGGCCCCGGAAATACAACCGTAGCGAGACTTACATCAGC	579
Oy	1186	GGCGGGGGCTTCCTGGCCCCGGAAGCTCAACCGCAGCGAGCGCTTACATCGCG	1236

RESULT 11
A1179632/C
11170623
E64 b0
CPNA 140000
ECST 08-TAN-10000

ACCESSION	
DEFINITION	EST223356 Normalized rat spleen, Bento Soares Rattus sp. cDNA clone
EST223356	Normalized rat spleen, Bento Soares Rattus sp. cDNA clone
RSPCJr1_3'	end, mRNA sequence.
A1179632	
VERSION	1
CT_A1179632	

KEYWORDS
SOURCE
ORGANISM
EST.
Rattus sp.
Rattus sp.
Pulkrutt
Metacoa. Chordata. Craniata. Vertebrata. Euteleostomi.

REFERENCE
Althoff
1 (bases 1 to 564)
Lee N H Gloder A Chandra I Mason T M Quackenbush J
Rattus
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

TITLE
Kerilavage, A.K. and Adams, M.D.
Rat Genome Project: Generation of a Rat EST Catalog & Rat
Gene Index
Unpublished (1998)

COMMENT: On Oct. 8, 1998 this sequence version replaced gi:3730270.
Contact: lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org

REFERENCE 1 (bases 1 to 1059)
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
 Plate: LNCM1794 row: m column: 18
 High quality sequence stop: 763.
 Location/Qualifiers
 1..1059
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4900793"
 /clone_lib="NIH-MGC_17"
 /tissue_type="rhodomyosarcoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: muscle; Vector: pOTB7; Site: 1: EcoRI; Site: 2: XhoI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(6). Site-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
 BASE COUNT 270 a 285 c 319 g 183 t 2 others
 ORIGIN
 Query Match 19.4%; Score 335.2; DB 10; Length 1059;
 Best Local Similarity 65.9%; Pred. No. 1.5e-53;
 Matches 540; Conservative 0; Mismatches 234; Indels 45; Gaps 2;

Db 443 CTTGTGTGAGAGGACCGAGGAGTACTGCGTGTGTAAGATCTTGGCAACTGACCGGCTA 502
 QY 1146 CGCCAGGACCTCTCCATGTGTGGGAGATCCCGACCGCGCGGCTTCTGTGGCGC 1205
 Db 503 TGGCAAGAGCTCTCCATGTGTGAGATCCCGACCGCGCGGCTTCTGTGGCGC 562
 QY 1206 GAAGCTCAACCGGAGGAGCTCTGAGATCCCGACCGCGGCTTCTGTGGCGC 1265
 Db 563 GAAGTTCACAAATCTGAGCAATACATGAGGAGGAGACATCTGTGTGACATTTCTT 622
 QY 1266 TGAGGCGCTCACTATGAGACCGTGGAGCAAGAGCGCTATGATGTGACAGCTGCT 1325
 Db 623 TGAAGTCTCACTATGAGACCATTTGAGCAAGAGCGCTATGATGTGACAGCTGCT 682
 QY 1326 TGGTGACATTTGGGGCCAGATGGGCTTTTATCTGCGGGCCAGCTGTCTACATCTCGA 1385
 Db 683 GGGTGAATGAGGGGCGCAAGATGGGCTGTATCTGCGGGCCAGATCTCTACAGGTCTGGA 742
 QY 1386 GATTCCTGACTACTCTGTGTGAGTGTTCGAGACAAAGT 1424
 Db 743 GCTCTTGTGACTAGCGCTACGAGGAGCATTAAGACAAAGT 781
 RESULT 14
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 LOCUS A1024055/c
 DEFINITION OV772C01.s1 Soares_testis.NHT Homo sapiens cDNA clone IMAGE:1642848
 3 similar to TR:035240 035240 PROTON GATED CATION CHANNEL DRASIC.
 ;, mRNA sequence.
 ACCESSION A1024055
 VERSION A1024055.1 GI:3239099
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (Bases 1 to 503)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 JOURNAL Tumor Gene Index
 COMMENT Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
 , Ph.D.
 DNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov/bdrip/image/image.html>
 www-bio.llnl.gov/bdrip/image/image.html
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 Seq primer: -40ml3 fwd. RT from Amersham
 High quality sequence stop: 137.
 location/Qualifiers
 1..503
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 /db_xref="taxon:9606"
 /clone="IMAGE:1642848"
 /clone_lib="Soares_testis_NHT"
 /sex="male"
 /lab_host="DH10B"
 /note="Vector: pT73D-pac (Pharmacia) with a modified polylinker; Site: 1: Not I; Site: 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - Oligo(dt) primer [5'] TGTACCAATCTGAAGTGGAGGCGCGCCCAATTTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization to Co5', and was constructed by Bento Soares and M. Fatima Bonaldo."
 BASE COUNT 101 a 135 c 157 g 110 t
 ORIGIN

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Query Match      18.9%; Score 326.8; DB 9; Length 503;
Best Local Similarity 84.6%; Pred. No. 66-52;
Matches 411; Conservative 0; Mismatches 2; Indels 73; Gaps 1;

OY 1236 GGAGAACGTGCTGGCCCTGGACATCTCTTTGAGGCCCTCAACTATGAGACCGTGAGCA 1295
    |||
DB 413 GGAGAACGTGCTGGCCCTGGACATCTCTTTGAGGCCCTCAACTATGAGACCGTGAGCA 354
    |||
OY 1296 GAAGAAGGCTATGAGATGTCAGAGCTGTTGTGACATTTGGGGGCGACATGGCCCTTTT 1355
    |||
DB 353 GAAGAAGGCTATGAGATGTCAGAGCTGTTGTGACATTTGGGGGCGACATGGGGCTGTT 294
    |||
OY 1356 CATCGGGGGCAGCCCTGCTCACCATCTCCAGATTCCTAGACTCTCTGAGAGTGTCCG 1415
    |||
DB 293 CATCGGGGGCAGCCCTGCTCACCATCTCCAGATTCCTAGACTCTCTGAGAGTGTCCG 234
    |||
OY 1416 AGACAAGTCTCTGGATTTTGTGAAACCGACAGCACTCCCAAGGCACTCCAGCACCA 1475
    |||
DB 233 AGACAAGTCTCTGGATTTTGTGAAACCGACAGCACTCCCAAGGCACTCCAGCACCA 174
    |||
OY 1476 TCTGCTCGAAGAGGCTGGGCGACCATGGAACCAAGTTCCCACTCAGCTGGGCC 1535
    |||
DB 173 TCTGCTCGAAGAGGCTGGGCGACCATGGAACCAAGTTCCCACTCAGCTGGGCC 114
    |||
OY 1536 CAGACCTCCACACCCTCCTCCTGTGCCGTACCAAGACTCTCTCGGCTCCACCGACCTG 1595
    |||
DB 113 ----- 114
    |||
OY 1536 CTACCTTGTACACAGCTCTAGACCTGCTGTGTCTCGAGGCCCGCCCTGACATC 1655
    |||
DB 113 ----- 67
    |||
OY 1656 CTGACATGCTCAGGCTGACGTAGCTTTTCCGTCTACCCCAATAAGCTCAATGC 1715
    |||
DB 66 CTGACATGCTCAGGCTGACGTAGCTTTTCCGTCTACCCCAATAAGCTCAATGC 7
    |||
OY 1716 ATCAAA 1721
    |||
DB 6 ATCAAA 1
    |||

RESULT 15
B1548575 835 bp mRNA linear EST 05-SEP-2001
LOCUS 603189513F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5260899 5',
DEFINITION mRNA sequence.
ACCESSION B1548575
VERSION B1548575.1 GI:15435887
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 835)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
http://image.llnl.gov
Plate: L1AM1657 row: j column: 04
High quality sequence stop: 831.
Location/Qualifiers
1..835
/organism="Homo sapiens"

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/db_xref="taxon:9606"
/clone="IMAGE:5260899"
/clone_id="NIH_MGC_95"
/tissue_type="hippocampus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pBluescript (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtagag
); Oligo-dr primed using primer 5'-TTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.5 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NIHRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT 167 a 282 c 229 g 157 t
ORIGIN

Query Match      18.8%; Score 325.6; DB 10; Length 835;
Best Local Similarity 98.8%; Pred. No. 1e-51;
Matches 328; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1150 AAGAGCTTCCATGCTGGGATCCCGAGCCGCCGCCGCTTCTGCCCCGGAAG 1209
    |||
DB 6 AAGAGCTTCCATGCTGGGATCCCGAGCCGCCGCCGCTTCTGCCCCGGAAG 65
    |||
OY 1210 CTCACCGCAGGAGCGCTACATCGCGGAGAGCTGTGCGCCCTGAGATCTTTTGAG 1269
    |||
DB 66 CTCACCGCAGGAGCGCTACATCGCGGAGAGCTGTGCGCCCTGAGATCTTTTGAG 125
    |||
OY 1270 GCCCTCAACTATGAGACCGGTGAGGAGAGAGGCTATGAGATGTCAGAGCTGCTG 1329
    |||
DB 126 GCCCTCAACTATGAGACCGGTGAGGAGAGAGGCTATGAGATGTCAGAGCTGCTG 185
    |||
OY 1330 GACATTTGGGGCGAATGGCCCTTTTCATCGGGGCGACCTGCTACCATCTCGAGATC 1389
    |||
DB 186 GACATTTGGGGCGAATGGGGCTTTTCATCGGGGCGACCTGCTACCATCTCGAGATC 245
    |||
OY 1390 CTGACATCTCTGTGAGAGTGTTCGAGACAAGTCTGTGGATTTTGTGAAACCGAG 1449
    |||
DB 246 CTGACATCTCTGTGAGAGTGTTCGAGACAAGTCTGTGGATTTTGTGAAACCGAG 305
    |||
OY 1450 CACTCCCAAGGCACTCCAGCACCAATCTGCT 1481
    |||
DB 306 CACTCCCAAGGCACTCCAGCACCAATCTGCT 337
    |||

Search completed: October 11, 2002, 04:18:56
Job time : 1974 secs

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QY 305 ACCCACTGCGCGCTGCGGCTTAAGCCCAACGACTGCACTGGGCTGCGCGCTGC 364
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 530 ATGCCCTGGGGTGTCCGACGCTACGCTACCTGCTCT--ACCTGGCCCATCAG 586
QY 365 TGGGCGCTGGATCCCGAGAGCAAGCGGCTTCCTGGCGCGCCCGCGCCCTGGAC 424
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 587 TAGGACTGGATGAGATGATGACCCCGGGGTGC-----CTTTCCTCTCTG 634
QY 425 CGCGCGGCTTCAATGCCCAGTCCACCTTTCACATGCGGCACTGATGCGCGTGGC 484
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 635 GCCCANAGGCTTTCCTCCGGGAGACCTTTTAACCTCCATCGTTTCTAATGCTCTTGC 654
QY 485 ACTCCCTGATGACATGCTGCTGGACTGTGCTTCGCTGGCCCAACTTGTGGGCTGAGA 544
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 695 ACCGCGTGGAGACATGCTGCTCTATTGTTCATGCTGGGGGCCCTCGGCTGCCACA 754
QY 545 ACTTCCACAGATCTTACCCTGGATGGGAAGTGTACACATTTAACTCTGGGCTGATG 604
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 755 ACTTCTCACTGTCTTCACTCGGTATGGGAAGTGTACACATTTCACTGGGCGCAAGATG 814
QY 605 GGGCAGAGCTGCTACACACTACTAGGGGTGGCATGGGCAATGGGCTGACATCATGCTGG 664
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 815 GCGCGGACAGGCTGAAGACCATGAAGGTGGGACTGGCAATGGCTGGAGATCATGCTGG 874
QY 665 ACGTGCAGAGAGAGAAATCTACTCTGTGTGAGAGCAATGAGAGACCCCTTTGAGG 724
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 875 ACATTCAGCAAGATGAATTTTCTGTGTGGGAGAGACCCGACGACATCTCTGGAAG 924
QY 725 TGGGGATCCGAGTGCAGATCCACAGCAGAGAGACCCCATCATGATCACTGGCTG 784
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 935 CAGGCACTCAAGATGCAATCCACAGTCAAGATGACACCCCTTTCATGACCACTGGGCT 994
QY 785 TGGGGGTGTCCCGGCTACACACTTGTTCCTGCGCAGCAGCAGCATGAGCTTGC 844
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 995 TTGGTGTGGCTCCAGGTTTCAGACCTTTGTGTCTTGGCAGAGGACAGAGGCTATCTACC 1054
QY 845 TGCACACGCGCTGGGGCGATGTCAGTCTCTGAACCCCACTATGAGCCAGAGC 904
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1055 TGCCTTCACCTGGGGCAGCTCGAATGCTGTTCACATGAGCTGGATTT----- 1103
QY 905 CCTGTGATCCCTAGGCTCCCGCAGCCCAAGCCCTCCCTATACCTTATGGGCT 964
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1104 -----CTTTCACCTCTACACATCACTGCGCT 1129
QY 965 GTGCGCTGCGCTGCGAAGCCCGCTACGTGCTCGAAGTGGGCTCGCAATGGTGTACA 1024
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1130 GCGCGATTAATTCGAGAGCGGCTTACTGTGTGAGAACTGCAACTCCGTATGTGTACACA 1189
QY 1025 TGCAGAGCGAGTGGCAGTGTGACGCCCGCAGCATGACAAAGAACTGTGCCACCGGCA 1084
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1190 TGCAGAGGAGCGCCCATCTGACTGCAGAGCATGACAAAGAGTGTGAGATCTGTGCC 1249
QY 1085 TAGATGCCATCTCT-----TGCAGAGACTCGTGGCGCTGGCCCAACCCGTGGCCAGCA 1138
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1250 TGGACTCTCTAATGAGAAAGACCAAGAACTGCTGTGTGAGATGCTTGTGCAACCTGA 1309
QY 1139 CGCGCTACCGCAAGAGCTCTCATGCTGCGATCCGAGACCGCGCGCGCGCTTTC 1198
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1310 CCGCGTACGCGCAAGAGCTGTCTCATGTCAAGATCCCAAGCAAGAGCTCCGCCAATTACC 1369
QY 1199 TGGCCCGGAGCTCAACCGCAGCGAGGCTACATCGCGGAGAAAGTGTGGCCCTGGACA 1258
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1370 TGGCGCAAGAAAGTCAACAATCGAGACATGATAGGGGAGAAACATTTGTGTCTGGACA 1429
QY 1259 TCTTCTTTAGAGCCCTCAACTATGAGACCGGTGAGAGCAAGAAAGGCTTATGAGATGTCA 1318
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1430 TTTTCTTTTGAATCTCTCAACTATGAGACCATGAGCAAGAAAGGCTTATGAGATGTCA 1489
QY 1319 ACCTGCTTTGACATTTGGGGCGAGATGGGCTTTTCACTGGGGCGCAGCTGCTGACACA 1378
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1490 GCGTGTGGGTGACATCGGGGGCGAGATGGGTTGTTCATCGGTGCGACATCTCTACCG 1549
QY 1379 TCCTCGAGATCTAGACTCTCTGTGTGAGGTGTTCGAGACAAAGTCTCGGATATTTCT 1438
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Db 1550 TGTGGAACCTTTTGAATATGCTTACAGAGTCAATTAAGCACAGGCTGTGCAGACGTGGAA 1609
QY 1439 GGAACGAGACGACTCCCAAGGCACTCCAGACACCAATCGCTTCAGAAAGGCGTGGCA 1498
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1610 AGTGCCAGAAAGAGGCTTAAGAGAGCAGCCAGACAAAGGCGGTGGGCTTCAGCTGATG 1669
QY 1499 GCCATGAAACCAAGTTTCCCACTCAGCTTGCGGCCAGACCTCCACCCCTGCTGTG 1558
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1670 ACGTCAAAAGACACAATCCCTGCGAGAGGCTCCGAGACATCTGCGGGATGACCTAG 1729
QY 1559 CCGTCAACA 1567
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1730 CTGCGCAACA 1738
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RESULT 4
US-09-360-197-3
; Sequence 3, Application US/09360197
; Patent No. 6287859
; GENERAL INFORMATION:
; APPLICANT: Bassilana, Frederic
; APPLICANT: Lazdunski, Michel
; APPLICANT: Waldehn, Rainer
; APPLICANT: Dewelle, Jan R.
; TITLE OF INVENTION: Human and Rat Families of Neuronal Acid-Sensitive
; TITLE OF INVENTION: Cationic Channels, Their Cloning and Applications
; FILE REFERENCE: 989,6706P
; CURRENT APPLICATION NUMBER: US/09/360,197
; CURRENT FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: 09/129,758
; PRIOR FILING DATE: 1998-08-05
; PRIOR APPLICATION NUMBER: 60/095,408
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: CDS
; NAME/KEY: CDS
; LOCATION: (1)..(1542)
US-09-360-197-3
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Query Match 26.4%; Score 456.8; DB 4; Length 1620;
Best Local Similarity 58.5%; Pred. No. 5.5e-99;
Matches 893; Conservative 0; Mismatches 567; Indels 66; Gaps 3;

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QY 69 CATCCGCTGTTCGCCAGCAACTGTCGATGCAAGGCTGGGCAAGTCTTGGGCGCAG 128
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9 CATCCAGGCGCTTCCGACGAGCTCCACACTGACAGGSCATGGCCACATCTTCTCTACGA 68
QY 129 CAGCTGAGCCTGCGCGCGGGGATGTGGCAGCGGCGCTGTCTCTGATGAGCCACTT 188
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 69 GCGGCTGTCTGTAAGCGGACACTGTGGGCGCTGTCTCTGAGGCTCTGCTGTGTGCT 128
QY 189 CCGTCAACAGGTGGCTGAGAGGCTGCGTACTACAGAGGATTCACACAGAGCTGCCCT 248
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 129 GCTGTGTGTGACAGGAGCGTGTGAGTACTACTTCCACTACAGCTGTGACACAGCT 188
QY 249 GGAATGCGAGAAAGCCACCGGCTGCTTCCGGCTGTACACCTGTGCAACATCAACC 308
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 189 CGACGAGGTGGCTGCTCTCAGCTTACCTTCCCTGTGTGACAGCTGTGCAACCTCAACA 248
QY 309 ACTGCGCGCGCTGCGGCTTAAAGCCCAAGCACTGCACTGGGCTGGGCTGTGCGCTG- 363
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 249 GTTCCGCTTTAGCAAGTCTCCAAAGATGACCTGTATCATGTGGGAGACTGCTGCGCT 308
QY 364 -----CTGGGCGCTGATCCCGAGAGCAAGCGCGGCTTCTGCGGCGCT 407
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 309 GCTCAACAACAGTATGAGATACAGACACACAGATGSCAGATGAAMAGCTGGAGAT 368
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OY	502	CTGCTGAGACTCTCCGCTTCCGTCGGCCAACTCTTGCGCTGAGAACTTCCACACAGATCTTC	561
Db	627	CTGCTCTGTGTGCACATTCCTCGTGGGGAGBGCCTGCAGCGCTGAAATTTCAAGTGTGTTC	686
OY	562	ACCCGATGGGAAAGTGTACACATTTAACTGTGCGCTGATGGGGCAGAGCTCTCAC	621
Db	687	ACTCGTATGGGAAAGTGTATTCACATTTCAACTCGGGCCAAAGTGGGGCCGACCGCTCAAG	746
OY	622	ACTACTAGGGTGGCATGGGCAATGGGCTGACATCTGCTGGACGTGCAGCAGAGAGAA	661
Db	747	ACCATGAAGGTGGGACTGCGCAATGGCCTGGAGATCATGTGGCACTTTCAGCAAGATGAA	806
OY	682	TATCTACCTGTGTGGAGGGACAATAGAGAGACCCCGTTTGAAGTGGGGATCCAGATGAC	741
Db	807	TATTTGCCCTGTGTGGGGAGAGAACCGAGAGACATCTTCCAGAGAGGCATCAAAAGTGCAG	866
OY	742	ATTCACAGCCCAAGAGAGAGCCGCCATCATGTGATACGTGGGCTTGGGGGTGTCCCGGGC	801
Db	867	ATCCACACTCAGAGATGAACCCCTTTTATGTGACACGCTGGGCTTGTGTGGCTCCAGGT	926
OY	802	TACCGACCTTGTGTTCTTTCGTGCACAGAGAGCTGAGCTTCGCGCACCGCCCTGGGGC	861
Db	927	TTCCAGACGTTTGTGTCTTGTGCCAGAGACAGAGCTCATTTACTGTGCCCTTACCTTGGGC	986
OY	862	GATTGCAGTTACGATCTGTGAACCCCACTGATAGGACAGAGCCCTGTGATCCCTAGGC	921
Db	987	ACCTTCATGCTGTTTACCATGATGATCGGATTT-----	101
OY	922	TCCCCACGCCCCAGCCCGCCCTCATATACCTTATGGGGTGTGCCCTGCGCTCGAA	981
Db	1019	-----CTTGACTCTTCAACAGCATCACTCCTCGCGGATTCGAGTTGTCGAG	106
OY	982	ACCCGCTACGTGCGTCCGGAAGTGGCTGGCGAATGCTGTACATATGCCAGCGAGCTGCACA	104
Db	1062	ACGGGTATCCTGTGTGGAGAACTGCACATGCGCATATGTTGTGACATATGCCAGGGAGGCCCA	112
OY	1042	GTGTGCAGCCCCCAGCAGTACAGAACTGTGCCACCCGGCCATATAGTCCATCT-----	109
Db	1122	TACTGCACCTCCAGAGCAGTACAAAGAGATGTGCAGATCTCCTCGGACTTCTCATGTGGAG	118
OY	1098	--TGCAGAGACTGTGGCGGCTGGCCCCCAACCCGTGGCCAGCAAGGGCTTCGCAAGAG	115
Db	1182	AAAGACCAAGAAATACTGCTGTGTGTGAATGCTTTGCAACTGCACCGCTTACGCAAGAG	124
OY	1156	CTTCTCATGTGTGCGGATCCGAGCCGCGCGCGGCTTCTGTGGCCCGGAAGCTCAAC	121
Db	1242	CTGTCTCAATGGTCAAGATCTCCAGCAAAAGCCTCGCCCAATGACTGTGGCAAGATTTCAAC	130
OY	1216	CGCAGCGAGGCTCATCTACGTGGGGAACGTCTGTGGCCCTGTGACATCTTTTGAAGGCCATC	127
Db	1302	AAATTCGAGCACTACATTAAGGGGAACATCTGTGTGTGACATTTCTTTGAAGTCTTC	136
OY	1276	AACTATGAGACCGTGGAGCAGAAAGAGCCCTATGAGATGTGCAGAGCTGCTTGTGCATTT	133
Db	1362	AACTATGAGACCATTCAGAGCAAGAAAAAGCCTATGAGATTCGACAGGCGCTTGGGTGATATC	142
OY	1336	GGGGGGCAGATGGGGCCTTTTCATGTGGGGCCAGCCTGCTACACATCTCTCGAGATCTAGAC	139
Db	1422	GGGGGGCAGATGGGGGTTTCTATCGGTGTCAGCATCTCTCAACGCTGTGGAACCTTTTGCAC	148
OY	1396	TACCTCTGTGAGGTGTTCACAGACAAAGTCTCTGGGATATTTCTGAAACCGACAGCACTCC	145
Db	1482	TATGTCTTACAGAGTCAATTAAGCAACAGGCTGTGCAGAGCTGGAAATGTGCCAGAAAGAGGCT	154
OY	1456	CAAAAGCACTTCACAGCAACCAATCTGTCTTTCAGAAAGGGCTGGGCAAGCCATGCAAACCAATT	151
Db	1542	AAGAGAGACACCGCAGACAAAGGGCGTGTGGCTCATGCTCTGATGATCACTCAAAAGACCAAT	160
OY	1516	CCCCACACAGCCCTGGGGCCCAAGACCTTCCACCCCTCCGTGTGCGGTGCACCA	1567
Db	1602	CCCTGTGAGAGCCCTCCGAGAGCAATCTGTGGCGGATGACAGTCACTCTCCACAA	1653

Query Match	Best Local Similarity	Score	DB 4	Length
Matches 842; Conservative 0; Mismatches 523; Indels 72; Gaps	58.68;	416.2;	DB 4;	1666;
US-09-360-197-5				
; Sequence 5, Application US/09360197				
; Patent No. 6287859				
; GENERAL INFORMATION:				
; APPLICANT: Bassilana, Frederic				
; APPLICANT: Lazdunski, Michel				
; APPLICANT: Waldmann, Rainer				
; APPLICANT: Dewille, Jan R.				
; TITLE OF INVENTION: Human and Rat Families of Neuronal Acid-Sensitive				
; TITLE OF INVENTION: Cationic Channels, Their Cloning and Applications				
; FILE REFERENCE: 989, 6706P				
; CURRENT APPLICATION NUMBER: US/09/360,197				
; CURRENT FILING DATE: 1997-07-23				
; PRIOR APPLICATION NUMBER: 09/129,758				
; PRIOR FILING DATE: 1998-08-05				
; PRIOR APPLICATION NUMBER: 60/095,408				
; PRIOR FILING DATE: 1998-08-05				
; NUMBER OF SEQ ID NOS: 22				
; SOFTWARE: PatentIn Ver. 2.1				
; SEQ ID NO 5				
; LENGTH: 1666				
; TYPE: DNA				
; ORGANISM: Homo sapiens				
; FEATURE:				
; NAME/KEY: CDS				
; LOCATION: (128)..(1663)				
US-09-360-197-5				
Query Match	24.08;	Score 416.2;	DB 4;	Length 1666;
Best Local Similarity	58.68;	Pred. No. 2.1e-89;		
Matches 842; Conservative 0; Mismatches 523; Indels 72; Gaps				
20 CCATGAAGCCACCTCAGAGCCAGAGAGCCCGGCGAGCCCTCGACATCCGCTGT	79			
126 CGATGACCTCAAGAAAGCCCGCAGTGAAGGCGACCTGCACTTTCAGCATCCAGATCT	185			
80 TCGCCAGCAATCGTCGATGACGAGGCGTGGCGACGTCCTTGGGCGCAGGCGCTGAGCC	139			
186 TTGCCAACACCTCCACCTCCATGACATCGCCACATCTTGTGTATGAGGCGCTGACCA	245			
140 TCGCCGGGGGATGTGGGCGAGCGGCGCGTGTCTGTGAGTGGCCACCTTCTTACACAG	199			
246 TCGCGCGTGTGTCGTGGGCGAGTGGCGCTTCGTTGGGCGTCTGTGGGCGTGTGGTGA	305			
200 TGGCTGAGAGGGTGGCGCTACTACAGGAGTTCCACACACAGACTGCGCTTGATGAGGAG	259			
306 GCTCTGAGAGGGGTGCTTACTACTTCTCTACACAGCATGTCCATGAGGTGAGCAGATGG	365			
260 AAAGCAGCGCGCTGCTTCCGGCTGTACACCGTGCATATCAACCCACTGGCGCGT	319			
366 TGGCTCAAGAGCTGTGTCTTCCAGCTGTGACCTCTGTATCTAATGAGCTTCCGTTCT	425			
320 CGCGCTTAAGCGCCCAAGACACTGCACTGGGCTGGGTCTGGCGTGGCTTGATCCG	379			
426 CCAGGCTCACCAACAGACACTGTATCATGCTGGGAGAGTGTGCGCCCTCTGGATGTCA	485			
380 CAGAGCAGCGCGCTTCTGTGG-----CGCCCTGGGCGGCGCCCTCTGCAC	424			
486 ACCTGCAATATCCCGAGCCCCCATCTGTGCTGACCCCTCGTGTGAGAGCCCTGGGCGACA	545			
425 CGCCCGGCTTATGCTCCAGTCCACCC-----TTTGATATGAGGCGCAACTGTATGCGCGT	478			
546 AGGCCAATTTACAGACACTACAAACCCCAAGCAAGTTCCAGACTGTCTGAGATTTCTCGACCGTG	605			
479 CTGGGCACTCCCTGGATGACATGTCTGTGAGCTGTGCTTCCGTGGCGCAACTTGTGGGC	538			
606 TGGGCACTGACCTGAAGGATGTGATGTCTCTACTGCAAGTTCAAAAGGCGAGAGATGGCGGC	665			
539 CTGAGAACTTACCAACGATCTTTCACCCGAGTGGAAAGTGCTACACTTAACTCTGGCG	598			
666 ACCAAGACTTTCACCAAGTGTTTTCAAAATATGGAAGTGTATGATGTTTAACTGACGGCG	725			

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OY 599 CTGATGGGAGAGAGCTGCTACCACTAGAGGGTGGCATGGGCATGGGCTGAGATCA 658
    ||||| | ||||| ||||| | ||||| ||||| ||||| ||||| ||||| |||||
Db 726 AGATGGAACAACTCTGCTACCAAGGAGGGGGAGAGGAGGAGGCTGGAGATCA 785
OY 659 TGTGAGACGTGCAGAGAGAAATATCTACCTGTGTGGAGGACATGAGAGACCCCTG 718
    ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 786 TGTGAGACATTTGAGAGAGATGAGTACTGCGCATCTGGGAGAGAGAGAGAAAGCAT 845
OY 719 TTGAGTGGGGATCCAGTCCAGATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 778
    ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 846 TTGAAGAGAGAGTGAAGAGTCAAGATCCAGATGATGAGTCAAGTCAAGAGAGAG 905
OY 779 TGGGCTGGGGGTGTCCCGGGGTACAGAGCTTTGTTTTCGACAGAGAGAGAGAGAG 838
    ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 906 TGGGCTTTGGGGGTGCTCCAGGGTTCAGAGCTTTGTTGTCACAGAGAGAGAGAGAG 965
OY 839 GCTTCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 898
    ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 966 CATACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1021
OY 899 CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 958
    ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1022 -----TTTCTGTTTACAGCATCA 1040
OY 959 TGGGGTGTGCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1018
    ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1041 CCGGCTGTAGAGATGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1100
OY 1019 TGTACATGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1078
    ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1101 TTGACATGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1160
OY 1079 CGGCTATGATGCCATCTTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1132
    ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1161 CTGCTGAGAGTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1220
OY 1133 CCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1192
    ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1221 ACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1280
OY 1193 GCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1252
    ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1281 AGTACCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1340
OY 1253 TGTGACATCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1312
    ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1341 TGTGATATATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1400
OY 1313 TGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1372
    ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1401 TGTGCTGCTTACTGTGTGATATGTGTGATGAGAGAGAGAGAGAGAGAGAGAGAG 1460
OY 1373 TCACCATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1429
    ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1461 TTGCAATACTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1517
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ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,596
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/626,838
FILING DATE: 02-Apr-1996
ATTORNEY/AGENT INFORMATION:
NAME: Nepal, Heidi S.
REGISTRATION NUMBER: 37,719
REFERENCE/DOCKET NUMBER: uif n6-53
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-288-3667
TELEFAX: 515-288-1338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1539 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1536
US-08-828-596-1

Query Match      24.0%; Score 415.8; DB 2; Length 1539;
Best Local Similarity 58.6%; Pred. No. 2,6e-89;
Matches 84; Conservative 0; Mismatches 522; Indels 72; Gaps 4;

OY 22 ATGAGGCCCACTGAGGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 81
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Db 1 ATGAGACCTCAAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
OY 82 GCCAGCAATCTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 141
    ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 GCCAACACTTCCAGCTTCCAGTGCATCCGACATCTTCTGTATGAGAGAGAGAGAGAGAG 120
OY 142 CGCCGGGAGATGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 201
    ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 CGGCGTGTGCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
OY 202 GCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 261
    ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 TCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
OY 262 AGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 321
    ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 GCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
OY 322 CGCCTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 381
    ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 AGGCTTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
OY 382 GAGCA-----CGCCGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 431
    ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 CTGAGAGATCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
OY 432 CTTATAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
    ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 421 GCCAACTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
OY 481 GGGCAGCTCCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
    ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 481 GGCATGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
    ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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QY	541	GAGAACCTTACACAGATCTTACCCGGATGGGAAAGTGCATCAACATTTAACCTCTGGCGCT	600
Db	541	CACAGCTTCCACCAAGATGTTTACAAATATATGGAGAGTTTACATGTTTAATCTAGCGCGAG	600
QY	601	GATGGGCGAGAGCTGCTACCACTACTAAGGGGTGGCATGGGCAATGGGCTGGACATCATG	660
Db	601	GATGGCAAACTCTGCTACACCGGTCAGAGGGGGGACAGCAACGGGCTGGAGATCATG	660
QY	661	CTGGACCTGGCAGCAGAGAGAAATATCTACCTGTGTGGAGGGACAATAGAGAGACCCGTTT	720
Db	661	CTGGACATCTACGAGAGATGATGATACCTCCCATCTGGGGGAAGACAGAGGAACGACATTTT	720
QY	721	GAGGTGGGGATCCCAAGTGCAGATCCACAGCCAGAGAGAGCGGCCCATCATGATCAGCTG	780
Db	721	GAACAGAGAGTGAAGAAATTTAGATCCACAGTACAGTGTAGGCACTTTTATCCAAAGAGCTG	780
QY	781	GGCTTGGGGGTGTCCCGGGCTACCAAGACTTTGTGTTTCTTGCAACGACAGCACTGTAGC	840
Db	781	GGCTTTTGGGGGTGTCCAGGGTTTCCACACCTTTGTGGCCACACAGAGGAGAGAGGCTTACA	840
QY	841	TTCTCTGCGACCGCCCTGGGGCGATTTGAGTTGACGATCTGTGAACCCCAACTATGAGCCA	900
Db	841	TACCTGCCCCACCGTGGGGGTGATGGCCATCCACAGAAATGGGGCTTCGACTTT-----	894
QY	901	GAGCCCTCTGATCCCTTAGGCTCCCCAGGCCCAAGCCCCAGCCCTCCTCATACCTTATG	960
Db	895	-----TTCTCTGTTTACACATCACTACCC	915
QY	961	GAGGTGGCCGTGGGCTGCGAAACCCGTAGCTGGCTGGGAAGTGGCGGTCGGAATGGTG	1020
Db	916	GGCTGTAGAGATTGCTGTGAGACCCGCTACATTTGTGGAAATCTGCACATCGCCGATGGTT	975
QY	1021	TACATGCCAGGCGAGCTGCCAGTGTGCAAGCCCCCAGCAGTACCAAGAACTGTGCCACCCG	1080
Db	976	CACATGCCAGGGGATGTGCCCTTTTGTGACCCCTGAGACGACCAAGAGTGTGAGAGCCGT	1030
QY	1081	GGCATAGATGCCATCTTCCGAGGAC-----TCTGTGGCCCTGGCCCCCAACCCGCTGCGCC	1130
Db	1036	GCCCTAGGCTCTGTTGGGCGGAAAGACAGCAATTAATCTGTCTGACAGAACCTCTCTCAAC	1090
QY	1135	AGCAGCGGCTACGCCAAGAGAGCTTCATGATGGTGTGCCGAGCGCGCGCGCGGCGC	1190
Db	1096	CTAACCCGCTACACAAAGAGCTTCCTCATGTGAAAGTCCCCAGCAAGACATCAGGCAAG	1150
QY	1195	TTCTCTGGCCCGGAGGCTCAACCCGACGAGCGCTACATCGCGAGAAAGTGTGCTGCGCTG	1250
Db	1156	TACCTTGAAGAAATTTAACTCAATTCAGAAATATATCTCACAAGAACATCTCTGTTCTG	1210
QY	1255	GACATCTCTTGAAGGCCCTCAACTATGACACCGTGGAGCGAGAAAGAGGCTATGAGATG	1310
Db	1216	GATATATATTTTGAAGCTCTCAATTTATGADACATTTGACAGAAAGAGGCGTATGAAATT	1270
QY	1315	TCAGAGCTGCTTGGTGAATTTGGGGGCGAGATGGGCTTTTCAATCGGGGCGACCTGCTC	1370
Db	1276	GCTCCTTACTTGTGATATTTGGGTCGACATGGGATGTGTTCAATTTGGTGTACTATCTTT	1330
QY	1375	ACCATCTCCAGATCTTAGACTACTCTGTGAGAGTGTTCGGAACAAGATCTCTGG	1429
Db	1336	ACAATCTAGAGGCTTGTGATATATATTTAATTAAGCTGATCAAAAGAGAGCTATATTAG	1390

```

RESULT 8
US-09-360-197-11
; Sequence 11, Application US/09360197
; Patent No. 6287859
;
; GENERAL INFORMATION:
;
; APPLICANT: Bassiliana, Frederic
;
; APPLICANT: Lazdunski, Michel
;
; APPLICANT: Waldmann, Rainer
;
; APPLICANT: Dewelle, Jan R.
;
; TITLE OF INVENTION: Human and Rat Families of Neuronal Acid-Sensitive
;
; TITLE OF INVENTION: Cationic Channels, Their Cloning and Applications

```

```

FILE REFERENCE: 989.6706P
CURRENT APPLICATION NUMBER: US/09/360,197
CURRENT FILING DATE: 1997-07-23
PRIOR APPLICATION NUMBER: 09/129,758
PRIOR FILING DATE: 1998-08-05
PRIOR APPLICATION NUMBER: 60/0055,408
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 1948
TYPE: DNA
ORGANISM: rattus sp.
FEATURE:
NAME/KEY: CDS
LOCATION: (16)..(1704)
US-09-360-197-11

```

Query Match	20.3%;	Score 352.2;	DB 4;	Length 1948;
Best Local Similarity	56.6%;	Pred. No. 2.9e-74;		
Matches 815;	Conservative 0;	Mismatches 533;	Indels 93;	Gaps 5

QY	37	GGCCAGAGGAAGAGCCCGGGGGGCGACGCCCTTGAGCATCCGGCTGTGCGCCAGCAACTGCTCG	96
Dp	163	GGGCGACGGGGTTCGCCCGCCAGGGGGGGCCGCTCCCTGAGTCGCACCTAAATTGCACGGGGCTG	222
QY	97	ATGCACGGGCTGTGGGCCACGCTCTTCTGGGGCCAGGACGCTAGCCCTGGCCGGGGAGATGTG	156
Dp	223	CGGCACATATGTGGCGGGGGCGACGGGGGGGGAGGGCTTTTCCAGGAGCAGGGGGCGTGTG	282
QY	157	GCAGCGGCCGCTGTGCTGTCACTGTGGCCACCTTCCTCTACCAAGTGGCTCAGAGGGTGGCC	216
Dp	283	GTGCGGGCCCTTGTGACGCTCCCTGGGCTTGGCTGTCTCTGTCTCCGCAACGCCGCTGTCTC	342
QY	217	TACTACAGGAGATCTCCACACCAACAGACTGGCCCTGGATGAGCAGAAAGACCGCGGCTGTCTC	276
Dp	343	TACTGGCTCAGCTTCCCGTCACACACACAGAGTGCACACCTGAGTGGAGAGCCGCGACGTCGCCG	402
QY	277	TTCCCGGCTGTACCCCTGTGCACATCAACCCACTGCGCGCGCTCGCCCTTAACGCCCAAC	336
Dp	403	TTCCCCCGCGTCAACGCTGTGCAACAAACCCCTTCGCTCCCGCGGCTCTTCCACAAGGG	462
QY	337	GACCTGCACATGGGGCTGGGCTGCGCTGCTGGCGGCGCTGGAATCC-----CGCAGACAG	388
Dp	463	GACCTCTACTACGCGGGCCACCTGGCTAGGGGTGCTGCTTCCCAACCGCACCGCGCGCCG	522
QY	389	CCGCGCTTCCCGCGGCCCGCCGCGGCCCGCCCTGCACCGCC-----	428
Dp	523	CTGTGTCACGAGACTGTCTGGGGGGCCACAGACCGCGCCGCTAGTGTTCGCGCAACTGTGCC	582
QY	429	-----CGGCTTCATGCCCCAGTCCCACTTTGA-----CATGGCGCACTTATVGGC	474
Dp	583	GACCTTCCGCTCTCTGCTGGCGCGCGGCCCACTTCGAGGGATCAGGCGCTCCTTCATGGAC	642
QY	475	CGTGTGGGCACTCCCTGGATGATCATGTGCTGTGGAGTGTGCGTTCGCTGGCCAACTTGT	534
Dp	643	CGTTTGGGCGCAACACTGGAGATATGTGCTCTCTCTGGAATACCGGGGCGAGCTCTGT	702
QY	535	GGGCGCTGAGCACTTACCAACAGATCTTTCACCCCGATGGGAAAGTCACTTAACTCT	594
Dp	703	GGCCCGCACTTCTCTCTCACTGTTTACAAATACGGGAAGTGTTCATGTTTAACTCA	762
QY	595	GGCGCTGATGGGGGAGAGCTGCTACCACTACTAGGGGTGGGCAATGGGCGTGGAC	654
Dp	763	GGCGAGAGATGGGAACCCGCTGCTACACAGCTCAAGGGGGGAGCGGGCAACGGGCTGGAG	822
QY	655	ATCATCTGTGACAGTGCACAGGAGGAAATATCTTACCTGTGTGAGGAGCAATGAGGACCC	714
Dp	823	ATCATGCTGTGACATTCACAGCAAGATGATGATCTGCCCATCTGGGGAGAGACAGAGGAACA	882
QY	715	CCGTTTGAAGTGGGATCCGAGTGCAGATCCACAGCCAGGAGAGACCCGCCATCATCGAT	774
Dp	883	ACGTTTGAAGCAGAGGTCAAGGTTTCAAGTTCACAGCTCATGCTGACCGCGCTTTCATCCAA	942

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QY 775 CAGTGGGCTGGGGGTGTCGCCGGCTACAGACCTTTGTTTCTTGCCAGCAGCAG 834
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 943 GAGCTGGCTTGGGGTGGCTCCGGGTTCCAGACCTTGTGGCCACACAGAGCAGAG 1002
QY 835 CTGAGCTTCTGCGCACCGCCCTGGGGCGATTGTCAGATCTCTGAAACCCACTAT 894
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1003 CTCACATATCTGCCCCCACCACATGGGGGAGTGCGCGGTCTCTCAGAGATGGGACTCGACT-- 1060
QY 895 GAGCCAGAGACCTCTGATCTCCTTGGCTCCCGACCCCAAGCCCTCCCTATACC 954
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1061 -----TCTTCTCTGTTTACAGC 1077
QY 955 CTTATGGGCTGCGCTGCGCTGCGAACCCTGCTAGCTGGCTGGAGTGGCGCTCCCA 1014
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1078 ATCACAGCTGTGGATTGATGTGAGACCCGCTACATGTGAGAACTGTAATCTCCG 1137
QY 1015 ATGTGTACATGCGACAGCGCTGCGAGTGTGACGCCCGCCAGCATGACAACTGTGCC 1074
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1138 ATGTGTACATGCGACAGCGCGCTTCTGTGACCCCTGAGAGACACAGAGTGTGCA 1197
QY 1075 CACCGGCGCATGATGCAATCCTTGCAGAGAC-----TCGTGCGCTGCCCAACCG 1128
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1198 GAGCCTGCGCTGCTACTGTCAGAAAGACAGCAATTAATGCTGTGACAGACACCC 1257
QY 1129 TGGCGCAGAGCGGCTAGCGCAAGAGCTCTCCATGTGCGATGCCGAGCGCGCGCC 1188
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1258 TCGAACCTGACAGCTACAAAGAGCTCTCCATGTGTAAGTTCGCCAGACAGCTCA 1317
QY 1189 GCGCGCTTCTGCGCGGAGAGCTCAACCGCAGGAGCTTACATCGCGAGAACTGTCTG 1248
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1318 GCGAGTACTTAGAGAGAAATTTAACAATGGAATAATATATCTCAGAGAACTATCT 1377
QY 1249 GCCCTGAGCATCTTCTTAGAGCGCTCAACTATGAGACCGTGGAGAGAGAGGCTAT 1308
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1378 GTTCTGAGCATATTTTGTAGGCGCTCAATTAAGAAATTAAGAAAGAGGCTAT 1437
QY 1309 GAGATGACAGCTGCTGTGATGATGAGTGGGGCGCAGATGGGCTTTCATCGGGGCGCAG 1368
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1438 GAGATGCTGCGCTTACTGTGTGACATGCGTGGTGGCAGATGGAGTGTTCATGCTGTAG 1497
QY 1369 CTGCTCACCATCTCGAGATCTGATGATCTGTGAGTGTTCGAGACAGAGTCTGT 1428
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1498 CTCCTCAGATACTAGAGCTCTTGTATTAATTTATGAGCTGATCAAGAGAACTATTA 1557
QY 1429 G 1429
Db 1558 G 1558

```

```

RESULT 9
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

```

```

APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300,6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PTZgpt-F1s
US-08-232-463-14

```

```

Query Match 2.9%; Score 50.4; DB 1; Length 7218;
Best Local Similarity 4.0%; Pred. No. 0.0086;
Matches 15; Conservative 210; Mismatches 151; Indels 0; Gaps 0;

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QY 1323 GCTTGTGATGATGGGGGCGAGATGGGCGCTTTTCATCGGGGCGAGCGCTGCATACCTG 1382
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1037 GCTTGTGATGATGGGGGCGAGATGGGCGCTTTTCATCGGGGCGAGCGCTGCATACCTG 1096
QY 1383 CGAGATCTAGATCTCTGTGAGTGTTCGAGACAGAGTCTGGATATTTCTGGA 1442
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1097 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1156
QY 1443 CCGACAGCACTCCCAAGGCACTCCAGACCAATCTGCTTACAGAAAGGCTGGGCGACCA 1502
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1157 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1216
QY 1503 TCGAACCAAGTCCCGCCTCCAGCAGCTGAGCTGGGCGCCAGACCGCCGCTGCGCTG 1562
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1217 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1276
QY 1563 CACCAAGACTCTCTCCGCTCCAGCAGCACTGCTACTGTTCACAGCTGAGACTG 1622
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1277 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1336
QY 1623 CTGTCTGTGCTCGAGACCGCGCTGACATCTGTGAGATGCTTACGCTGACGTAAGCT 1682
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1337 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1396
QY 1683 TTTCCGCTTCACCCC 1698
Db 1397 YYYYYYYYYYYYYY 1412

```

```

RESULT 10
US-08-997-080-133
; Sequence 133, Application US/08997080
; Patent No. 5968524
; GENERAL INFORMATION:
; APPLICANT: WATSON, JAMES D.
; APPLICANT: TAN, PAUL L.J.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA

```

```

: COUNTRY: USA
: ZIP: 98121
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/997,080
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Sleath, Janet
: REGISTRATION NUMBER: 37,007
: REFERENCE/DOCKET NUMBER: 11000.1007
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 206-269-0565
: TELEFAX: 206-269-0563
: TELEX:
: INFORMATION FOR SEQ ID NO: 133:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 742 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: Genomic DNA
:
US-08-997-080-133

```

```

Query Match          2.5%; Score 43.8; DB 2; Length 742;
Best Local Similarity 49.4%; Pred. No. 0.15;
Matches 114; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

OY 1088 ATGCATCTTCGCGAAGACTGTCGCGCTGCCCCCAACCCGTGGCCGACGCGGCTACG 1147
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 368 AGGGGATCGCGCTTGACAGACCGCGCGACGCGCGCTGTCGCCGCCCAATGCCAGAT 427

OY 1148 CCAAGAGACTCTCCATGATGTCGGATCCGAGCCGCGCGCGCGCTTCCTGGCCCGGA 1207
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 428 TCAACGAGTTCTTCCCGGAGATCGTGACACCGCTTCACATTGAGAGATGTGATGCTGCG 487

OY 1208 AGCTCAACCGCAGGAGCGCTACATCGCGGAGAACGTGCTGCGCCCTGGACATCTTCTTTG 1267
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 488 ACCTCGAGGAGACGTGTGTACTCGCGCTACAAAGGGCGGATCTCGGGCAAAACATCG 547

OY 1268 AGGCCCTCACTATGAGACCGCTGAGCAGAAAGAGCCCTATGAGATGTGAG 1318
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 548 TCAACGGCCCTATCGCAACCGGAGAACTGTGGAAGCCTACGAGAAAGCGG 598

```

```

RESULT 11
US-08-997-362-133
: Sequence 133, Application US/08997362
: Patent No. 5985287
: GENERAL INFORMATION:
: APPLICANT: Tan, Paul
: APPLICANT: Hiyama, Jun
: APPLICANT: Visser, Elizabeth
: APPLICANT: Skinner, Margot
: APPLICANT: Prestidge, Ross
: TITLE OF INVENTION: TREATMENT AND METHODS FOR MYCOBACTERIAL INFECTIONS
: NUMBER OF SEQUENCES: 194
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Law Offices of Ann W. Speckman
: STREET: 2601 Elliott Avenue, Suite 4185
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98121

```

```

: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/997,362
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
: FILING DATE: June 12, 1997
: APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
: FILING DATE: August 29, 1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Sleath, Janet
: REGISTRATION NUMBER: 37,007
: REFERENCE/DOCKET NUMBER: 11000.1002c2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 206-269-0565
: TELEFAX: 206-269-0563
: TELEX:
: INFORMATION FOR SEQ ID NO: 133:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 742 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: Genomic DNA
:
US-08-997-362-133

```

```

Query Match          2.5%; Score 43.8; DB 2; Length 742;
Best Local Similarity 49.4%; Pred. No. 0.15;
Matches 114; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

OY 1088 ATGCATCTTCGCGAAGACTGTCGCGCTGCCCCCAACCCGTGGCCGACGCGGCTACG 1147
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 368 AGGGGATCGCGCTTGACAGACCGCGCGACGCGCGCTGTCGCCGCCCAATGCCAGAT 427

OY 1148 CCAAGAGACTCTCCATGATGTCGGATCCGAGCCGCGCGCGCGCTTCCTGGCCCGGA 1207
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 428 TCAACGAGTTCTTCCCGGAGATCGTGACACCGCTTCACATTGAGAGATGTGATGCTGCG 487

OY 1208 AGCTCAACCGCAGGAGCGCTACATCGCGGAGAACGTGCTGCGCCCTGGACATCTTCTTTG 1267
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 488 ACCTCGAGGAGACGTGTGTACTCGCGCTACAAAGGGCGGATCTCGGGCAAAACATCG 547

OY 1268 AGGCCCTCACTATGAGACCGCTGAGCAGAAAGAGCCCTATGAGATGTGAG 1318
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 548 TCAACGGCCCTATCGCAACCGGAGAACTGTGGAAGCCTACGAGAAAGCGG 598

```

```

RESULT 12
US-09-095-855-133
: Sequence 133, Application US/09095855
: Patent No. 6160093
: GENERAL INFORMATION:
: APPLICANT: Tan, Paul
: APPLICANT: Visser, Elizabeth
: APPLICANT: Skinner, Margot
: APPLICANT: Prestidge, Ross
: TITLE OF INVENTION: Compounds and Methods for Treatment and Diagnosis of Mycobacterial Infections
: NUMBER OF SEQUENCES: 208
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Law Offices of Ann W. Speckman
: STREET: 2601 Elliott Avenue, Suite 4185
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98121
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette

```

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,855
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,347
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 23-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000,1002c3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
LENGTH: 742 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-09-095-855-133

Query Match 2.5%; Score 43.8; DB 4; Length 742;
Best Local Similarity 49.4%; Pred. No. 0.15;
Matches 114; Conservative 0; Mismatches 117; Indels 0; Gaps 0;
QY 1088 ATGCATCTTCCGCAAGAGCTGTCGCGCCCAACCCGTGCGCCAGACGCGCTACG 1147
DB 368 AGCGCATCGCGTTGCGAGACGCGCGGAGCGCGCGCTGTGCGCGCAATGCCAGAT 427
QY 1148 CCAAGAGCTCTCCATGATGTCGCGGATCCGACCGCGCGCGCTTCTGCGCGGA 1207
DB 428 TCAACGAGTCTTCCGCGAGATCGTCACCGCTTCAACTTCGAGATCGATCTGCTCG 487
QY 1208 AGCTCAACGCGAGCGGCTCATGCGGAGAGAGCGTGGCGCGGAGCATTTCTTGG 1267
DB 488 ACCTCGAGGCGACGCTGTGATCTCCGCTACAGGCGCGGATCTCGGACCAACATCG 547
QY 1268 AGCCCTCAACTATGAGACCGTGGAGCAGAGAAGGCTATGAGATGTCAG 1318
DB 548 TCAACGCGCCCTATCGCAACCGGGAAGTGTGGAAGCTATGAGAGAGCGCG 598

RESULT 13
US-09-324-542-133
Sequence 133, Application US/09324542
Patent No. 6328978
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L.J.
TITLE OF INVENTION: Methods and Compounds for the Treatment
FILE OF INVENTION: of Immunologically-Mediated Skin Disorders
FILE REFERENCE: 11000,1007c1
CURRENT APPLICATION NUMBER: US/09/324,542
CURRENT FILING DATE: 1999-06-02
EARLIER APPLICATION NUMBER: US 08/997,080
EARLIER FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 194
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 133
LENGTH: 742
TYPE: DNA
ORGANISM: Mycobacterium vaccae

US-09-324-542-133
Query Match 2.5%; Score 43.8; DB 4; Length 742;
Best Local Similarity 49.4%; Pred. No. 0.15;
Matches 114; Conservative 0; Mismatches 117; Indels 0; Gaps 0;
QY 1088 ATGCATCTTCCGCAAGAGCTGTCGCGCCCAACCCGTGCGCCAGACGCGCTACG 1147
DB 368 AGCGCATCGCGTTGCGAGACGCGCGGAGCGCGCGCTGTGCGCGCAATGCCAGAT 427
QY 1148 CCAAGAGCTCTCCATGATGTCGCGGATCCGACCGCGCGCGCTTCTGCGCGGA 1207
DB 428 TCAACGAGTCTTCCGCGAGATCGTCACCGCTTCAACTTCGAGATCGATCTGCTCG 487
QY 1208 AGCTCAACGCGAGCGGCTCATGCGGAGAGAGCTGCTGCGCTTCTGCGCATTTCTTGG 1267
DB 488 ACCTCGAGGCGACGCTGTGATCTCCGCTACAGGCGCGGATCTCGGACCAACATCG 547
QY 1268 AGCCCTCAACTATGAGACCGTGGAGCAGAGAAGGCTATGAGATGTCAG 1318
DB 548 TCAACGCGCCCTATCGCAACCGGGAAGTGTGGAAGCTATGAGAGAGCGCG 598

RESULT 14
US-08-997-080-122
Sequence 122, Application US/08997080
Patent No. 5968524
GENERAL INFORMATION:
APPLICANT: WATSON, JAMES D.
APPLICANT: TAN, PAUL L.J.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,080
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000,1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 898 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-08-997-080-122
Query Match 2.5%; Score 43.8; DB 2; Length 898;
Best Local Similarity 49.4%; Pred. No. 0.15;
Matches 114; Conservative 0; Mismatches 117; Indels 0; Gaps 0;
QY 1088 ATGCATCTTCCGCAAGAGCTGTCGCGCCCAACCCGTGCGCGAGACGCGCTACG 1147

Db 524 AGGCGATGCGCTTCGACGACGCGCGCGCGCGCTGCTGCGCCGCAATGCGAGAT 583
OY 1148 CCAAGAGCTCTCCATGATGGGATCCGAGCGCGCGCGCGCGCTTCCGCGCGCGGA 1207
Db 584 TCAACGAGTCTTCCGCGGATGTCGACCGCTTCACTTCAGAGATGATGCTGCG 643
OY 1208 AGCTCAACCGCAGCGAGCGCTTACATCGCGGAGAACGCTGCGCCCTGAGCATCTTCTTGG 1267
Db 644 ACCTCGAGGCGAACGTCGTGATCTCCGCTACAGAGGCGCGGATCTCGGAGCAAAACATCG 703
OY 1268 AGCCCTCACTATGAGACCGTCGAGCAGAGAACGCGCTATGATGTCAG 1318
Db 704 TCAACGCGCCCTATCGCAACCGGAACTGTCGGAAGCCTACGAGAAAGCGG 754

RESULT 15
US-08-997-362-122

Sequence 122, Application US/08997362
Patent No. 5985287
GENERAL INFORMATION:
APPLICANT: Tan, Paul
APPLICANT: Hiyma, Jun
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Scott, Linda
APPLICANT: Prestidge, Rosa
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
NUMBER OF SEQUENCES: 194
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,362
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
FILING DATE: June 12, 1997
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
FILING DATE: August 29, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Sleeth, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002c2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 898 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-08-997-362-122

Query Match 2.5%; Score 43.8; DB 2; Length 898;

Best Local Similarity 49.4%; Pred. No. 0.15; Mismatches 117; Indels 0; Gaps 0;

Matches 114; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

Search completed: October 11, 2002, 04:20:32
Job time : 109 secs

Db 524 AGGCGATGCGCTTCGACGACGCGCGCGCGCGCTGCTGCGCCGCAATGCGAGAT 583
OY 1148 CCAAGAGCTCTCCATGATGGGATCCGAGCGCGCGCGCGCGCTTCCGCGCGCGGA 1207
Db 584 TCAACGAGTCTTCCGCGGATGTCGACCGCTTCACTTCAGAGATGATGCTGCG 643
OY 1208 AGCTCAACCGCAGCGAGCGCTTACATCGCGGAGAACGCTGCGCCCTGAGCATCTTCTTGG 1267
Db 644 ACCTCGAGGCGAACGTCGTGATCTCCGCTACAGAGGCGCGGATCTCGGAGCAAAACATCG 703
OY 1268 AGCCCTCACTATGAGACCGTCGAGCAGAGAACGCGCTATGATGTCAG 1318
Db 704 TCAACGCGCCCTATCGCAACCGGAACTGTCGGAAGCCTACGAGAAAGCGG 754

Qy	1	MRPTSGDEARQCSDLRVFASNC	SMHGLGVFPGSLSRGMAAAVYLSVTFILQY	60
Db	1	MKPTSGDEARRASDLRVFASNC	SMHGLGVFPGSLSRGMAAAVYLSVTFILQY	60
Qy	61	AERYRYRREFHQTALDERESHRLV	PPAVYLCINPLRSLRFLPNDLHMG	120
Db	61	AERYRYRREFHQTALDERESHRLI	PPAVYLCINPLRSLRFLPNDLHMG	120
Qy	121	EHAFLRLALGRPPAPGPMSPPTF	DMOLVAKASHSLDDMLDLCRFQO	180
Db	121	EHAFLRLALGRPPAPGPMSPPTF	DMOLVAKASHSLDDMLDLCRFQO	180
Qy	181	TRMGKCYTENGADGAELITTRT	GMNGLIDIMLDVQOEXFLPWRDNEET	240
Db	181	TRMGKCYTENGADGAELITTRT	GMNGLIDIMLDVQOEXFLPWRDNEET	240
Qy	241	IHSDEEPIIDQLGLGVSFGYQTV	VSQQOOLSTLPPPMGDCSSASLNP	300
Db	241	IHSDEEPIIDQLGLGVSFGYQTV	VSQQOOLSTLPPPMGDCSSASLNP	300

[illegible]

```

RESULT 2
US-09-360-197-10
: Sequence 10, Application US/09360197
: Patent No. 6287859
: GENERAL INFORMATION:
: APPLICANT: Bassilana, Frederic
: APPLICANT: Lazdunski, Michel
: APPLICANT: Waldmann, Rainer
: APPLICANT: Dweville, Jan R.
: TITLE OF INVENTION: Human and Rat Families of Neuronal Acid-Sensitive
: TITLE OF INVENTION: Cationic Channels, Their Cloning and Applications
: FILE REFERENCE: 989.6706P
: CURRENT APPLICATION NUMBER: US/09/360,197
: CURRENT FILING DATE: 1997-07-23
: PRIOR APPLICATION NUMBER: 09/129,758
: PRIOR FILING DATE: 1998-08-05
: PRIOR APPLICATION NUMBER: 60/095,408
: PRIOR FILING DATE: 1998-08-05
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: Patentin Ver. 2.1
: SEQ ID NO 10
: LENGTH: 533
: TYPE: PRF
: ORGANISM: rattus sp.
US-09-360-197-10

```

Query Match	85.8%	Score 2447	DB 4	Length 533
Best Local Similarity	83.5%	Pred. No. 2e-234		
Matches 445	Conservative 49	Mismatches 37	Indels 2	Gaps 2

[illegible]

Dd	361	LKDDCVCPNCCATRYAKELSMYRIPSRASABATLARKYRNSESYITRENTVLVDIFREAL	420
Oy	419	NYEPPEOKKAYEMSELGDDIGGOMGLFIFGASLTLTLELFDLYCEVFDKVLGYFMWNRHS	478
Dd	421	NYEAVEGKAATVEVELDLDIGOGNGLFGISALTLTLBELDYLCEVDRVLGTFMWNRSA	480
Oy	479	ORHSNTNLDDGGLSHRQVPHLSLGRPPRPRAVYKTLSSHRCTYLTQOL	531
Dd	481	OKRSQNTLQDELNGHRTNPHVLSLGRPPPTPCAVKTLSSASRITYLTVALR	533

RESULT 3
US-08-828-596-2
; Sequence 2, Application US/08828596

```

1  GENERAL INFORMATION:
2  APPLICANT:  Welsh, Michael J.
3  APPLICANT:  Price, Margaret P.
4  TITLE OF INVENTION:  No. 5892018e1 Brain Sodium Channel Protein Family
5  TITLE OF INVENTION:  and DNA Sequences Encoding Same
6  NUMBER OF SEQUENCES:  5
7  CORRESPONDENCE ADDRESS:
8  ADDRESSEE:  Zarley, McKee, Thomte, Voorhees & Sease
9  STREET:  801 Grand Suite 3200
10 CITY:  Des Moines
11 STATE:  Iowa
12 COUNTRY:  United States
13 ZIP:  50309
14
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE:  Floppy disk
17 COMPUTER:  IBM PC compatible
18 OPERATING SYSTEM:  PC-DOS/MS-DOS
19 SOFTWARE:  PatentIn Release #1.0, Version #1.30
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER:  US/08/828,596
22 FILING DATE:
23 CLASSIFICATION:  435
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER:  US 08/626,838
26 FILING DATE:  02-APR-1996
27 ATTORNEY/AGENT INFORMATION:
28 NAME:  Nebel, Heidi S.
29 REGISTRATION NUMBER:  37,719
30 REFERENCE/DOCKET NUMBER:  ulif n6-53
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE:  515-288-3667
33 TELEFAX:  515-288-1338
34 INFORMATION FOR SEQ ID NO:  2:
35 SEQUENCE CHARACTERISTICS:
36 LENGTH:  512 amino acids
37 TYPE:  amino acid
38 TOPOLOGY:  linear
39 MOLECULE TYPE:  protein
40
41 US-08-828-596-2

```

Query Match	Score 1365;	DB 2;	Length 512;
Best Local Similarity	50.68;	Pred. No. 5.5e-127;	
Matches 255; Conservative	83;	Mismatches 140;	Indels 26; Gaps 5;

[illegible]

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Db 186 VFTKGYKCYMENSDEGDKPLLTYYKGTGNGLEIMLIDIOODEYLPIMGETTEETFEAGVK 245
Oy 239 VOIHSQEEPPPIIDOLGLGVSPGYOTFVSCQOOQLSFLPPMGDCSSASINPEPEPSDP 298
Db 246 VOIHSQSEPPPIOTGLGVAPGFOFVATQEOQLTYLPPMGECSSSEMGIDF----- 298
Oy 239 LGSPSPSPPYTYLMGCRACETRYVARKCGCRMYVMGDPVCSPOOYKNCAPADAI 358
Db 239 -----FPYISTACRIDCETRIYVENCRCRWYHMGDAPFCFPEQHKCEAPALGL 350
Oy 359 LKQDS--CACPNPCASTRYAKELSNVRIPSRARAFARKINRSBAYIAENVLALDIFE 416
Db 351 AEKDSNYCICRPPCMLTRYNKELSMVKIPSKTSAKYLEKFKSKYISENITLVIDIFE 410
Oy 417 ALNVTYEOKRAYEMSELLDGIQOMGLFIGASLTIIEILDYLCVEFRDXYLGFWMRQ 476
Db 411 ALNVTYEOKRAYEVALLDIGOMGLFIGASILTILEFDYIYELIKELLDLKEE 470
Oy 477 HSQRHSTNLLQEGLSHRTQVPH 500
Db 471 DEGSHDENVSTCDTPMNHSETISH 494

```

RESULT 4

```

US-09-360-197-6
: Sequence 6, Application US/09360197
: Patent No. 6287659
: GENERAL INFORMATION:
: APPLICANT: Bassilana, Frederic
: APPLICANT: Lazdunski, Michel
: APPLICANT: Waldmann, Rainer
: APPLICANT: Deweille, Jan R.
: TITLE OF INVENTION: Human and Rat Families of Neuronal Acid-Sensitive
: FILE OF INVENTION: Cationic Channels, Their Cloning and Applications
: FILE REFERENCE: 989, 6706P
: CURRENT APPLICATION NUMBER: US/09/360,197
: PRIOR FILING DATE: 1997-07-23
: PRIOR APPLICATION NUMBER: 09/129,758
: PRIOR FILING DATE: 1998-08-05
: PRIOR APPLICATION NUMBER: 60/095,408
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: Patentin Ver. 2.1
: SEQ ID NO 6
: LENGTH: 512
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-360-197-6

```

Query Match 47.9%; Score 1365; DB 4; Length 512;

Best Local Similarity 50.6%; Pred. No. 5.5e-127; Matches 253; Conservative 83; Mismatches 140; Indels 26; Gaps 5;

```

Oy 7 PEARROPSDIRVFAVNSCMHGLGHVFGPSLSLRGMAAAVLSVATFLYQVARY 66
Db 7 PSESSLGSSSIQIFANTSTLGHIRIIFVYGLTIRRVLAFAVSSGLGLLVESSESY 66
Oy 67 YREFHQTALDERESHRLVPAVTLCLNINPLRRSLTPNDLHMAGSALLGID-----PAE 121
Db 67 YFSYQHTVKEDEVVAQSLVPAVTLCLNINLNGFRFSRLTNDLYHAGELLALLDVLNQLPDP 126
Oy 122 HAA---FLRAGLRPPAPPGFMPSPFEDMAQLYARAGHSLDDMLDCRRRGQCGCEBNFTT 178
Db 127 HLADPSVLEALRQKANKFHYKPK-QFSMLEFLHRVGHDKMDMLCKFKGQCGHODFTT 185
Oy 179 IFTRMGCYTFNSGADGAELTTTRGGMGNGLDIMLVQOEEYLPVWRNDNEETPREVGIR 238
Db 186 VFTKGYKCYMENSDEGDKPLLTYYKGTGNGLEIMLIDIOODEYLPIMGETTEETFEAGVK 245
Oy 239 VOIHSQEEPPPIIDOLGLGVSPGYOTFVSCQOOQLSFLPPMGDCSSASINPEPEPSDP 298
Db 246 VOIHSQSEPPPIOTGLGVAPGFOFVATQEOQLTYLPPMGECSSSEMGIDF----- 298

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Oy 299 LGSPSPSPPYTYLMGCRACETRYVARKCGCRMYVMGDPVCSPOOYKNCAPADAI 358
Db 299 -----FPYISTACRIDCETRIYVENCRCRWYHMGDAPFCFPEQHKCEAPALGL 350
Oy 359 LKQDS--CACPNPCASTRYAKELSNVRIPSRARAFARKINRSBAYIAENVLALDIFE 416
Db 351 AEKDSNYCICRPPCMLTRYNKELSMVKIPSKTSAKYLEKFKSKYISENITLVIDIFE 410
Oy 417 ALNVTYEOKRAYEMSELLDGIQOMGLFIGASLTIIEILDYLCVEFRDXYLGFWMRQ 476
Db 411 ALNVTYEOKRAYEVALLDIGOMGLFIGASILTILEFDYIYELIKELLDLKEE 470
Oy 477 HSQRHSTNLLQEGLSHRTQVPH 500
Db 471 DEGSHDENVSTCDTPMNHSETISH 494

```

RESULT 5

```

US-09-360-197-8
: Sequence 8, Application US/09360197
: Patent No. 6287659
: GENERAL INFORMATION:
: APPLICANT: Bassilana, Frederic
: APPLICANT: Lazdunski, Michel
: APPLICANT: Waldmann, Rainer
: APPLICANT: Deweille, Jan R.
: TITLE OF INVENTION: Human and Rat Families of Neuronal Acid-Sensitive
: FILE OF INVENTION: Cationic Channels, Their Cloning and Applications
: FILE REFERENCE: 989, 6706P
: CURRENT APPLICATION NUMBER: US/09/360,197
: PRIOR FILING DATE: 1997-07-23
: PRIOR APPLICATION NUMBER: 09/129,758
: PRIOR FILING DATE: 1998-08-05
: PRIOR APPLICATION NUMBER: 60/095,408
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: Patentin Ver. 2.1
: SEQ ID NO 8
: LENGTH: 559
: TYPE: PRT
: ORGANISM: rattus sp.
US-09-360-197-8

```

Query Match 46.9%; Score 1337; DB 4; Length 559;

Best Local Similarity 49.8%; Pred. No. 3.8e-124; Matches 256; Conservative 82; Mismatches 142; Indels 34; Gaps 7;

```

Oy 1 MKPTSGPEARROPSDIRVFAVNSCMHGLGHVFGPSLSLRGMAAAVLSVATFLYQV 60
Db 47 MARGSELDGSDSPDDIYAFANSCTFHGASHVYFVGCGPRKALMAVAFYALGAFLOV 106
Oy 61 AERVYRYREFHQTALDERESHRLVPAVTLCLNINPLRRSLTPNDLHMAGSALLGIDPA 120
Db 107 GBRVAYLYSPHVTLDEAVATTELVEPAVTPCNTAVRLSOLSYDLYL-APMLGLDES 165
Oy 121 EHAALRLAGLRPPAPPGFMPSPFEDMAQLYARAGHSLDDMLDCRRRGQCGCEBNFTT 180
Db 166 DDPGVPLA---PPGEAFSGEP-FNLHRYNRSCHRLDMLLYCYCGPGCPHNFVSVF 221
Oy 181 TFMGCYTFNSGADGAELTTTRGGMGNGLDIMLVQOEEYLPVWRNDNEETPREVGIRQ 240
Db 222 TRYGCYTFNSGQDGRPRPKTYMKGTGNGLEIMLIDIOODEYLPVWGETDSEFEAGIRVQ 281
Oy 241 IHSQEEPPPIIDOLGLGVSPGYOTFVSCQOOQLSFLPPMGDCSSASINPEPEPSDPLG 300
Db 282 IHSQEEPPPIIDOLGLGVAPGFOFVATQEOQLTYLPPMGTCNAVYMDSD----- 332
Oy 301 SPSPPSPPYTYLMGCRACETRYVARKCGCRMYVMGDPVCSPOOYKNCAPADAIIR 360
Db 333 -----FDSYSTACRIDCETRIYVENCRCRWYHMGDAPCTPPOYECAADPADFLVE 386
Oy 361 KDS--CACPNPCASTRYAKELSNVRIPSRARAFARKINRSBAYIAENVLALDIFEAL 418

```

Db 387 KDOEQVCVEMCNCNLTFRGKELSNVTKIPFSKASAKYLAKFPKMSQYIGENILTVIDIFEVL 446

Qy 419 NYEYVEOKKAAVEMSELGIDGGONGGLTIGASILITLLEIYDLEFPNDKYLGTFMNRQHS 478

Db 447 NYETLEOKKATVEIAGLGDIGONGGLTIGASILTVLELFPYAEVYIKRRLC-----RRGKC 502

Qy 479 QRHSSTNLQDGLCSHRTQVPRHLSLGPFRPPPC 512

Db 503 QKEAKRSSADKGVA-----LSLDVYKRRNP 528

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RESULT 6
US-09-360-197-2
; Sequence 2, Application US/09360197
; Patent No. 6287859
; GENERAL INFORMATION:
; APPLICANT: Bassilana, Frederic
; APPLICANT: Lazdunski, Michel
; APPLICANT: Waldmann, Rainer
; APPLICANT: Dweille, Jan R.
; TITLE OF INVENTION: Human and Rat Families of Neuronal Acid-Sensitive
; TITLE OF INVENTION: Cationic Channels, Their Cloning and Applications
; FILE REFERENCE: 989 6706P
; CURRENT APPLICATION NUMBER: US/09/360,197
; CURRENT FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: 09/129,758
; PRIOR FILING DATE: 1998-08-05
; PRIOR APPLICATION NUMBER: 60/095,408
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 526
; TYPE: PRT
; ORGANISM: Rattus sp.
; US-09-360-197-2

```

[illegible]

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OY      474  NRQHSQRHSSTNLQEGLGSRHTQVPHSLGPREPTPC 512
          |  :  :  :  :  :  :  ||  ||
DB      465  RRGKCGQEAARKRSSADKVA-----LSLDDVYKRHNPC 495
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```

US-09-360-197-4
RESULT 7
US-09-360-197-4
Sequence 4, Application US/09360197
Patent No. 6287859
GENERAL INFORMATION:
APPLICANT: Bassilana, Frederic
APPLICANT: Lazduski, Michel
APPLICANT: Waldmann, Rainer
APPLICANT: Dewelle, Jan R.
TITLE OF INVENTION: Human and Rat Families of Neuronal Acid-Sensitive
TITLE OF INVENTION: Cationic Channels, Their Cloning and Applications
FILE REFERENCE: 989,6706P
CURRENT APPLICATION NUMBER: US/09/360,197
CURRENT FILING DATE: 1997-07-23
PRIOR APPLICATION NUMBER: 09/129,758
PRIOR FILING DATE: 1998-08-05
PRIOR APPLICATION NUMBER: 60/095,408
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 514
TYPE: PRT
ORGANISM: Homo sapiens
US-09-360-197-4

```

Query Match	46.3%	Score 1319;	DB 4;	Length 514;	
Best Local Similarity	49.2%	Pred. No. 2e-122;			
Matches 255;	Conservative 80;	Mismatches 129;	Indels 54;	Gaps 8	
QY 14	PSDIRVFASNC	SMGLGVF	GGPGLSLSR	GMVAALVSVATFLVQVAREVRYEFNHQ 73	
Db 1	PVSIDAFSSSLH	GMHAI	FYSERLSTLR	KALMALCFGLSIAVLVLCSTGRVQYFHHV 60	
QY 74	TALDERESHRLV	PAVAVTLC	INPLRSLR	LTLPDMLMAGS - -ALLG----- 116	
Db 61	TKLDEVAASQ	LFEPVAVTLC	INLNEFFSOVSK	KDYLHAEELALLNNRYEIPDTQADEKQ 120	
QY 117	LDPAEHAFLR	ALGRPAR	PGFMSPTE	DMQVLYRAGHSLDMLDLCRFRCOPCGPENE 176	
Db 121	LEIIDQKRN	NFMS -----	FKRP - ENMRFY	RAGHDIDMLLSCHFREVCSADEF 170	
QY 177	TTFTFMKCYT	FENSGAD	GAELTTT	RCGMGNGIDLIMLDVQOEYLVPWRDNEETPFEVG 236	
Db 171	KVFEFRVYKCY	TFNPSGR	NRGRLPK	TKMGKGTGNGLEIMLDIQDEYLLPVMGTFDEFSFEG 230	
QY 237	IRVQIHSEEP	RIIDQLG	YSPGVTIV	SCQOQDLSTLPPWAGCSASSLNLPNTEPEPS 296	
Db 231	IKVQIHSDDE	PPFIIDQL	GFVAPGFQ	TVACQEORLIYLPWMGCKAVTMDSDIDFSDS 290	
QY 297	DPLGSPSP	SPAPPT	YLMGCR	LACETRYAARCKGCMVWPGVPVPCSPQOYKNCAPHAD 356	
Db 291	-----	YSITACRID	CEFRYL	YVENCNCMMVHMPGADAPCTPEQYKECADPAID 337	
QY 357	AALRKDS --	CACPNE	CASTRAY	AKELSMVRI	DSRAARFLARKLNSEAYIAENVALDIEF 414
Db 338	FLVERDQGY	CVCBPC	NCNTRY	GKELSMVK	IRPSKASAKTLAKFNKNSBDQYIGNILVLDIEF 397
QY 415	FEALNFEV	EOKKAVE	KEMSELL	GDIGGQNG	LFIGASLLTILELTDLYLCEVFRDKVLGYFWN 474
Db 398	FEVNLNFEI	EOKKAVEI	IGLGDIG	GGQNGLE	FIGASILTIVLELFDYAYGVIKHKLC-----R 453
QY 475	RQHSQRHS	STMLOE	GLGSH	RTPVPHLS	LGRPPTRPC 512
Db 454	RGKQCKE	AKRRSS	ADKGA -	-----	LSLDVYKRRHPC 483

RESULT 8

US-09-360-197-12
 ; Sequence 12, Application US/09360197
 ; Patent No. 6287859
 ; GENERAL INFORMATION:
 ; APPLICANT: Bassilana, Frederic
 ; APPLICANT: Lazdunski, Michel
 ; APPLICANT: Waldmann, Rainer
 ; APPLICANT: Deweille, Jan R.
 ; TITLE OF INVENTION: Human and Rat Families of Neuronal Acid-Sensitive
 ; TITLE OF INVENTION: Cationic Channels, Their Cloning and Applications
 ; FILE REFERENCE: 989.6706P
 ; CURRENT APPLICATION NUMBER: US/09/360.197
 ; CURRENT FILING DATE: 1997-07-23
 ; PRIOR APPLICATION NUMBER: 09/129,758
 ; PRIOR FILING DATE: 1998-08-05
 ; PRIOR APPLICATION NUMBER: 60/095,408
 ; PRIOR FILING DATE: 1998-08-05
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: Patentln Ver. 2.1
 ; SEQ ID NO 12
 ; LENGTH: 563
 ; TYPE: PRT
 ; ORGANISM: rattus sp.
 US-09-360-197-12

Query Match 43.8%; Score 1249.5; DB 4; Length 563;
 Best Local Similarity 47.5%; Pred. No. 1.9e-115;
 Matches 245; Conservative 79; Mismatches 151; Indels 41; Gaps 8;

QY 6 GPEARR-OPSDIRVFNASCSMHGLGV-FCGSGSLRGMMAAVLVSVATFLYQVARYREFHQTAL 60
 DB 50 GCGVARRGPRP-----LSRKLHGLRHMCAGRTAGSGQRALAVLVAFCTSLGILLSMS 104
 QY 61 AERVYTYREFHQTALDERESHRLVPRVATLCINPLRSLRTPNDLMAGSALLGLDPA 120
 DB 105 SNRLTYWLSFSPHTVYHREWSKQLPFPVATYCNPNPLRPSLSKGLYYAGHMLGLLFPN 164
 QY 121 EHA-AFLRALGRPARPG-----FMSPTFD--MAQLYARAGSHLDDMLDCRF 166
 DB 165 RYARLVSEELRGDEPRKROWFRKLADFLPLRPHEGISAFFMDLQGLDMLLSCKY 224
 QY 167 RGQPCGPNFTTITRMGKCYTNSGADGAEILLTTTRGSGMGLDMLDVOOEYLPVWR 226
 DB 225 RGLCGPHNFSVFTKYGKCYMNSGDEGKPLTLTVKGTGMLDMLDIOQDEVLPING 284
 QY 227 DNEETPEFYGLVQHSQEPPIIDQLGVSPPGYQTFVSCQOOLSLPRPWGDCSSAS 286
 DB 285 ETEETTFEAGVYQHSQSEPPFIQLGFGVAPGFOTFVATQEORLTYLPPWGCDSSE 344
 QY 287 LNPNTPEPSDPLGSPSPSPRYTLMGCRACETRYVARKGCGRMYVMPGDPVPCSPQ 346
 DB 345 MGLD-----FPVYSITACRIDCETRYVENCGRMYVMPGDPVPCSPQ 389
 QY 347 YKNCAPADALIRKDS--CACPNPCASTRYAKELSMWRIPSRARAFIARKLNSEAVT 404
 DB 390 HKECAEPALGLIAEKDSNVCICRTPCNLTTRYKELSMWKIPKTSAKYIEKKFNSEKTI 449
 QY 405 AENVLADIFFEALNYEVEOKKAYEMSELLDGGOMGLTGASILLTLETLDYLCVEY 464
 DB 450 SENIILVLDIFFEALNYEVEOKKAYEMSELLDGGOMGLTGASILLTLETLDYIELI 509
 QY 465 RDKVLGYFMNRHQSRRHSSTNLQGLSGHRTQVPH 500
 DB 510 KEKLIDLLGKEEBSGSHDNMSTCDTPMNHSETTISH 545

RESULT 9
 US-09-360-197-15
 ; Sequence 15, Application US/09360197
 ; Patent No. 6287859
 ; GENERAL INFORMATION:
 ; APPLICANT: Bassilana, Frederic
 ; APPLICANT: Lazdunski, Michel

; APPLICANT: Waldmann, Rainer
 ; APPLICANT: Deweille, Jan R.
 ; TITLE OF INVENTION: Human and Rat Families of Neuronal Acid-Sensitive
 ; TITLE OF INVENTION: Cationic Channels, Their Cloning and Applications
 ; FILE REFERENCE: 989.6706P
 ; CURRENT APPLICATION NUMBER: US/09/360.197
 ; CURRENT FILING DATE: 1997-07-23
 ; PRIOR APPLICATION NUMBER: 09/129,758
 ; PRIOR FILING DATE: 1998-08-05
 ; PRIOR APPLICATION NUMBER: 60/095,408
 ; PRIOR FILING DATE: 1998-08-05
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: Patentln Ver. 2.1
 ; SEQ ID NO 15
 ; LENGTH: 625
 ; TYPE: PRT
 ; ORGANISM: Helix aspersa
 US-09-360-197-15

Query Match 14.7%; Score 419; DB 4; Length 625;
 Best Local Similarity 22.2%; Pred. No. 6.7e-33;
 Matches 136; Conservative 99; Mismatches 191; Indels 186; Gaps 20;

QY 17 IRVFASCSMHGLGVFCGSGSLRGMMAAVLVSVATFLYQVARYREFHQTAL 76
 DB 43 IAEIGSESNAGHLAKIVISRD-TKRKYVALLVINGFTATATQLSLVKRYLQFVVELS 101
 QY 77 DERESHRLVPRVATLCINPLRSLRTPNDLMAGSALLGLDPAEHAFLRA 128
 DB 102 EIKDSMPVQYRPSGSIENIPISLRTIRMYFNNESSQNLITWL--RFIOKFRFEOOSFMS 159
 QY 129 LGRPARPGFMSPPF--MAQLYARAGSHLDDMLDCRFROGCPGPNFTITF-RMK 185
 DB 160 I-----RAVEYELGODAKKLSHNLDMHCFNRELCHVSNEFTFGCNFTN 207
 QY 186 CYTFNSGADGAEILLTTTRGSGMGLDMLDVOOEYLP-----VMDNEETPREVGIRVOI 241
 DB 208 CTFNPG-----QRLDMHATGPNGLSLIFSVEKDEPLPCTGYVYFNDNLIHSAGVRYV 263
 QY 242 HSQEPPIIDQLGVSPPGYQTFVSCQOOLSLPRPWGDCSSASLN--PNYEPSDPL 299
 DB 264 HAPGSPSPFVDHGDIDIPGYSSVGLKAILHTRLPYPGYCNMDMLNGIKQYK----- 316
 QY 300 GSPSPSPRYTLMGCRACETRYVARKGCGRMYVMPGDPV----- 340
 DB 317 -----YTFACLOLCKQRLIIQRCGCKSSALP-EVPSYNATFCGVIKDQWEINRN 365
 QY 341 -----VCSPQOYKNCAPADALIRKDS--CACPNPCASTR 374
 DB 366 HSNEDHNOSEEDRAFIPTYLACEREOKN-----LNDRITYELSCGFQFCSETS 416
 QY 375 YAKELSMWRIP-----SRAARFIARKLNSEAVT 405
 DB 417 YLKSYSLSVWPLEFYQLSAVERFQEOBQAGNHFPAKTYEYLEKLHPSQHLARNSH 476
 QY 406 -----ENVLADIFFEALNYEVEOKKAYEMSELLDGGOMGLTGASILLTLETLDY 440
 DB 477 MDLILSKYSLSSEKEMAKASDLIRQNMRLNLYEDLSVEYEROLPAYGLADLRADJGG 536
 QY 441 OMGLFAGSALLTLETLDYLCVEFVRDQVLYGFWMNQ-----HSQRHS 482
 DB 537 TGLMKGISVLTIMELIELVY-----RLTGLVFNSEKGLRPGPTVYNNNGSNHNSQ-ST 590
 QY 483 STNLLQEGIGSH 494
 DB 591 SQHQLYNGYMDH 602

RESULT 10
 US-08-376-362A-20
 ; Sequence 20, Application US/08376362A
 ; Patent No. 5693756
 ; GENERAL INFORMATION:


```

; APPLICANT: Johnson, Carl D.
; TITLE OF INVENTION: HOMOLOG CLONING
; NUMBER OF SEQUENCES: 142
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/861,458C
; FILING DATE: 04/01/92
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04585/014001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 753
; TYPE: amino acid
; TOPOLOGY: linear
;
US-07-861-458C-98
Query Match 11.9%; Score 338.5; DB 4; Length 753;
Best Local Similarity 27.2%; Pred. No. 8.9e-25;
Matches 106; Conservative 56; Mismatches 137; Indels 91; Gaps 14;

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; Patent No. 6232061
; GENERAL INFORMATION:
; APPLICANT: Marchionni, Mark Andrew
; TITLE OF INVENTION: HOMOLOG CLONING
; NUMBER OF SEQUENCES: 142
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/861,458C
; FILING DATE: 04/01/92
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04585/014001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 520
; TYPE: amino acid
; TOPOLOGY: linear
;
US-07-861-458C-100
Query Match 11.2%; Score 320; DB 4; Length 520;
Best Local Similarity 22.2%; Pred. No. 3.5e-23;
Matches 121; Conservative 61; Mismatches 178; Indels 184; Gaps 19;

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Db 393 AINPNI GADCPAYVHISNDSKACAEYRRLNTAYIEIYEQINPFTLKEFTAGYTLVNLPSD 452
QY 438 IGGOMGLEFI GASLFTLEILDYLC EV-----FRDKVIGYFWMROHSQHSSTN 485
Db 453 FGGNIGIMIGFSVYTMFEVVEVLCEI IYIGTHSLFKLFSKLL-----PSQENNHATA 505
QY 486 LLOE 489
Db 506 FINE 509

Search completed: October 11, 2002, 08:11:12
Job time : 35 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2002, 04:20:40 : Search time 88 Seconds
(without alignments)
1043.867 Million cell updates/sec

Title: US-09-530-233-2
Perfect score: 2851
Sequence: 1 MKPTSGPEARROPDIRVF.....CAVTKTLSASHRTCYLVTLQ 531

Scoring table:
BLASTSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2851	100.0	531	4 075906	075906 homo sapien
2	2833	99.4	531	4 090ER8	090ER8 homo sapien
3	2768.5	97.1	542	4 060263	060263 homo sapien
4	2706	94.9	549	4 090HC3	090HC3 homo sapien
5	2598	91.1	543	4 090HC4	090HC4 homo sapien
6	2447	85.8	533	11 035240	035240 rattus norv
7	1367	47.9	512	11 0925H0	0925H0 mus musculu
8	1340	47.0	513	11 088762	088762 rattus norv
9	1339	47.0	559	11 091YB8	091YB8 rattus norv
10	1247.5	43.8	563	11 051633	051633 rattus norv
11	1247.5	43.8	563	11 061203	061203 mus musculu
12	1180	41.4	539	4 090M04	090M04 homo sapien
13	1169	40.9	539	11 090H56	090H56 rattus norv
14	1167	40.9	539	11 090YV9	090YV9 rattus norv
15	1130.5	39.7	4	096FT7	096FT7 homo sapien
16	1037	36.4	425	11 099NA1	099NA1 rattus norv

17	987	34.6	309	13 057657	057657 fugu rubrip
18	791.5	27.8	347	4 096CV2	096CV2 homo sapien
19	631	22.1	495	11 090RY1	090RY1 mus musculu
20	625	21.9	495	11 090RW5	090RW5 rattus norv
21	616	21.6	505	4 090Y37	090Y37 homo sapien
22	495	17.4	198	11 097811	097811 mus musculu
23	411	14.4	632	5 09BJD0	09BJD0 lymnaea sta
24	405.5	14.2	622	5 09NHC7	09NHC7 heliosoma tr
25	400.5	14.0	557	5 091835	091835 caenorhabdi
26	398	14.0	682	11 09RLN2	09RLN2 cavia cobya
27	391	13.7	656	11 090XF9	090XF9 cavia porce
28	372	13.0	646	5 001664	001664 caenorhabdi
29	350	12.3	649	4 096TD2	096TD2 homo sapien
30	349	12.2	663	5 091100	091100 caenorhabdi
31	338	11.9	638	5 091115	091115 caenorhabdi
32	309	10.8	629	5 091102	091102 caenorhabdi
33	307.5	10.8	302	6 09N009	09N009 ovis aries
34	298	10.5	608	5 091103	091103 caenorhabdi
35	288.5	10.1	613	5 022970	022970 caenorhabdi
36	287.5	10.1	334	6 09N118	09N118 ovis aries
37	266.5	9.3	643	5 045402	045402 caenorhabdi
38	264.5	9.3	599	5 018077	018077 caenorhabdi
39	263.5	9.2	355	6 09N133	09N133 oryctolagus
40	248.5	8.7	548	5 09VAJ7	09VAJ7 drosophila
41	247.5	8.7	516	5 09V7S4	09V7S4 drosophila
42	230.5	8.1	516	5 061365	061365 drosophila
43	230.5	8.1	516	5 061370	061370 drosophila
44	229.5	8.0	602	5 09VS73	09VS73 drosophila
45	227	8.0	595	5 09VME9	09VME9 drosophila

ALIGNMENTS

RESULT 1
ID 075906 PRELIMINARY; PRT: 531 AA.
AC 075906:

DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PRORON-GATED CATION CHANNEL SUBUNIT.

OS ASIC3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OC NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA TISSUE=BRAIN;

RA TISSUE=KIDNEY; K. T. Seguela P.

RT Genotyping, functional properties and distribution of a non-

RT degenetizing proton-gated channel from human brain.

RL Submitted (APR-1998) to the EMBL/Genbank/DBJ databases.

DR EMBL: AF057711; AAC62935.1; -

DR Interpro: IPR001873; ASC.

DR Pfam: PF00858; ASC; 1

DR SEQUENCE 531 AA; 58930 MW; 71C7C31A1A1ED9D CRC64;

Query Match 100.0%; Score 2851; DB 4; Length 531;
Best Local Similarity 100.0%; Pred. No. 3e-253;
Matches 531; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKPTSGPEARROPDIRVFASNSMGHGFPGPSLSLRGMAAAVYLSATPTLYOY 60
|||||
DB 1 MKPTSGPEARROPDIRVFASNSMGHGFPGPSLSLRGMAAAVYLSATPTLYOY 60
QY 61 AERVRYYREFHNOTALDESHRLVPAVTLCLINPLRSRLTPNDLHWAGSALLGLDPA 120
|||||
DB 61 AERVRYYREFHNOTALDESHRLVPAVTLCLINPLRSRLTPNDLHWAGSALLGLDPA 120
QY 121 EHAALFALGRPPAPPGFMSPTFDMAQLYARAGSLDMLDCCRFGPCGPFENFTTF 180
|||||

```

Db 121 EHAFLRALGRRPAPPGFMPSPTEFDMALYARAGHSLLDMLDCRRFQPCGPNFTTIF 180
OY 181 TRMGKCYTFNSGADGAEILLTTTRGCMGNGLDIMLDVQOEELPYVRDNEETPEFVGIRVQ 240
Db 181 TRMGKCYTFNSGADGAEILLTTTRGCMGNGLDIMLDVQOEELPYVRDNEETPEFVGIRVQ 240
OY 241 IHSQEEPIIDQLGLGVSFGYQTFVSCQOQOQSLFLPPWGDSSASLNPNEPEPSDPLG 300
Db 241 IHSQEEPIIDQLGLGVSFGYQTFVSCQOQOQSLFLPPWGDSSASLNPNEPEPSDPLG 300
OY 301 SPSPSPSPPTLMGCRCLACETRYVARCKGCRMYMPGDPVPCSPQOYKNCAHPAIDALIR 360
Db 301 SPSPSPSPPTLMGCRCLACETRYVARCKGCRMYMPGDPVPCSPQOYKNCAHPAIDALIR 360
OY 361 KDSCACPNPCASTRYAKELSWRIPSRRAARFLARKLNSEAYIAENVALDIFEALNY 420
Db 361 KDSCACPNPCASTRYAKELSWRIPSRRAARFLARKLNSEAYIAENVALDIFEALNY 420
OY 421 ETEQCKKAYEMSELLGDIQGGOMGLFTIGASLLTILEILDYLCVFRDKVLGYFWRNQSQR 480
Db 421 ETEQCKKAYEMSELLGDIQGGOMGLFTIGASLLTILEILDYLCVFRDKVLGYFWRNQSQR 480
OY 481 HSTNLDEGLGSHRTQVPHLSLGRPPTPCAVTKTLSASHRTCYLTOL 531
Db 481 HSTNLDEGLGSHRTQVPHLSLGRPPTPCAVTKTLSASHRTCYLTOL 531

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RESULT 2

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OY 09098 PRELIMINARY: PRT: 531 AA.
AC 09098:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE PROTON-GATED CATION CHANNEL ASIC3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96416055; PubMed=9744806;
RA de Welle J.R., Bassilana F., Lazdunski M., Waldmann R.;
RT "Identification, functional expression and chromosomal localisation of
RT a sustained human proton-gated cation channel.";
RL FEBS Lett. 433:257-260(1998);
DR EMBL, AF095897; AAC64188.1;
DR InterPro; IPR001873;
DR Pfam; PF00858;
DR PRINTS; PRO1078; AMINCHANNEL.
SQ SEQUENCE 531 AA; 58905 MW; A46D64590EC4871 CRC64;

```

Query Match 99.48% Score 2833; DB 4; Length 531;
 Best Local Similarity 99.28; Pred. No. 1.4e-251;
 Matches 527; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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OY 1 MKPTSGPEEAROPSDIVFASNCMGLGVFGPGLSLRGMMAAVALVSVATFLYQV 60
Db 1 MKPTSGPEEAROPSDIVFASNCMGLGVFGPGLSLRGMMAAVALVSVATFLYQV 60
OY 61 AERYVRYREFHHQALDERESHRLVPAVTLCTNINPLRSLRTPNDLHMAGSALLGLDPA 120
Db 61 AERYVRYREFHHQALDERESHRLVPAVTLCTNINPLRSLRTPNDLHMAGSALLGLDPA 120
OY 121 EHAFLRALGRRPAPPGFMPSPTEFDMALYARAGHSLLDMLDCRRFQPCGPNFTTIF 180
Db 121 EHAFLRALGRRPAPPGFMPSPTEFDMALYARAGHSLLDMLDCRRFQPCGPNFTTIF 180
OY 181 TRMGKCYTFNSGADGAEILLTTTRGCMGNGLDIMLDVQOEELPYVRDNEETPEFVGIRVQ 240
Db 181 TRMGKCYTFNSGADGAEILLTTTRGCMGNGLDIMLDVQOEELPYVRDNEETPEFVGIRVQ 240
OY 241 IHSQEEPIIDQLGLGVSFGYQTFVSCQOQOQSLFLPPWGDSSASLNPNEPEPSDPLG 300

```

```

Db 241 IHSQEEPIIDQLGLGVSFGYQTFVSCQOQOQSLFLPPWGDSSASLNPNEPEPSDPLG 300
OY 301 SPSPSPSPPTLMGCRCLACETRYVARCKGCRMYMPGDPVPCSPQOYKNCAHPAIDALIR 360
Db 301 SPSPSPSPPTLMGCRCLACETRYVARCKGCRMYMPGDPVPCSPQOYKNCAHPAIDALIR 360
OY 361 KDSCACPNPCASTRYAKELSWRIPSRRAARFLARKLNSEAYIAENVALDIFEALNY 420
Db 361 KDSCACPNPCASTRYAKELSWRIPSRRAARFLARKLNSEAYIAENVALDIFEALNY 420
OY 421 ETEQCKKAYEMSELLGDIQGGOMGLFTIGASLLTILEILDYLCVFRDKVLGYFWRNQSQR 480
Db 421 ETEQCKKAYEMSELLGDIQGGOMGLFTIGASLLTILEILDYLCVFRDKVLGYFWRNQSQR 480
OY 481 HSTNLDEGLGSHRTQVPHLSLGRPPTPCAVTKTLSASHRTCYLTOL 531
Db 481 HSTNLDEGLGSHRTQVPHLSLGRPPTPCAVTKTLSASHRTCYLTOL 531

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RESULT 3

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ID 060263 PRELIMINARY: PRT: 532 AA.
AC 060263:
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE SODIUM CHANNEL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS.
RX MEDLINE=96238685; PubMed=9571199;
RA Ishibashi K., Marumo F.;
RT "Molecular cloning of a DEG/ENAC sodium channel cDNA from human
RT testis";
RL Biochem. Biophys. Res. Commun. 245:589-593(1998).
DR EMBL; AB010575; BAA25897.1;
DR InterPro; IPR001873;
DR Pfam; PF00858;
SQ SEQUENCE 532 AA; 59154 MW; B84CB4A1ACAD02FB CRC64;

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Query Match 97.18% Score 2768.5; DB 4; Length 532;
 Best Local Similarity 97.08; Pred. No. 1.2e-245;
 Matches 516; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

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OY 1 MKPTSGPEEAROPSDIVFASNCMGLGVFGPGLSLRGMMAAVALVSVATFLYQV 60
Db 1 MKPTSGPEEAROPSDIVFASNCMGLGVFGPGLSLRGMMAAVALVSVATFLYQV 60
OY 61 AERYVRYREFHHQALDERESHRLVPAVTLCTNINPLRSLRTPNDLHMAGSALLGLDPA 120
Db 61 AERYVRYREFHHQALDERESHRLVPAVTLCTNINPLRSLRTPNDLHMAGSALLGLDPA 120
OY 121 EHAFLRALGRRPAPPGFMPSPTEFDMALYARAGHSLLDMLDCRRFQPCGPNFTTIF 180
Db 121 EHAFLRALGRRPAPPGFMPSPTEFDMALYARAGHSLLDMLDCRRFQPCGPNFTTIF 180
OY 181 TRMGKCYTFNSGADGAEILLTTTRGCMGNGLDIMLDVQOEELPYVRDNEETPEFVGIRVQ 240
Db 181 TRMGKCYTFNSGADGAEILLTTTRGCMGNGLDIMLDVQOEELPYVRDNEETPEFVGIRVQ 240
OY 241 IHSQEEPIIDQLGLGVSFGYQTFVSCQOQOQSLFLPPWGDSSASLNPNEPEPSDPLG 300
Db 241 IHSQEEPIIDQLGLGVSFGYQTFVSCQOQOQSLFLPPWGDSSASLNPNEPEPSDPLG 300
OY 301 SPSPSPSPPTLMGCRCLACETRYVARCKGCRMYMPGDPVPCSPQOYKNCAHPAIDALIR 359
Db 301 SPSPSPSPPTLMGCRCLACETRYVARCKGCRMYMPGDPVPCSPQOYKNCAHPAIDALIR 360

```

```

OY 360 KDCSCAPNCASTRYAKELSMVRIPSRARFLARKLNRESEAYIAENVLADLFFFEALN 419
    |||||||
DB 361 KDCSCAPNCASTRYAKELSMVRIPSRARFLARKLNRESEAYIAENVLADLFFFEALN 420
OY 420 YETVEOKKAYEMSELLDGGOMGLFSGASLTLTLEILDYLCVEFRDKVLGYFWMRQHSQ 479
    |||||||
DB 421 YETVEOKKAYEMSELLDGGOMGLFSGASLTLTLEILDYLCVEFRDKVLGYFWMRQHSQ 480
OY 480 RRSSTNLQEGLSHRTQVPHLSLGRPPPTPCAVTKTLSASHRTCYLVTOI 531
    |||||||
DB 481 RRSSTNLQEGLSHRTQVPHLSLGRPPPTPCAVTKTLSASHRTCYLVTOI 532

```

RESULT 4

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OY 090HC3 PRELIMINARY: PRT; 549 AA.
AC 090HC3;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE ACID SENSING ION CHANNEL 3 SPLICE VARIANT C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Renard S., Besnard F., Partiseti M., Graham D.;
RT ASIC3b a new member of the acid sensing ion channel family ";
RL Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF195025; AAF19818.1; -
DR InterPro: IPR001873; ASC.
DR Pfam: PF00858; ASC; 1.
DR PRINTS: PRO1078; AMINACHANNEL.
SQ SEQUENCE 549 AA; 60491 MW; ED2C4D628AF9E18F CRC64;

```

Query Match 94.9%; Score 2706; DB 4; Length 549;

Best Local Similarity 93.9%; Pred. No. 6,7e+240; Matches 511; Conservative 3; Mismatches 14; Indels 16; Gaps 2;

```

OY 1 MKPTSGPEEARROPSDIRVFASNCNMHGLGHVFGPSLSLRGMMAAAVLSVATFLYOV 60
    |||||||
DB 1 MKPTSGPEEARROPSDIRVFASNCNMHGLGHVFGPSLSLRGMMAAAVLSVATFLYOV 60
OY 61 AERVRYRREHHQTALDERESHRLVFPAYTLNINPLRSRLPNLHMAGSALLGLDPA 120
    |||||||
DB 61 AERVRYRREHHQTALDERESHRLVFPAYTLNINPLRSRLPNLHMAGSALLGLDPA 120
OY 121 EHAALFLALGRPPAPPGFMPSPTFDMAOLYARAGHSLDMLDCRRGQPCGPEFTTIF 180
    |||||||
DB 121 EHAALFLALGRPPAPPGFMPSPTFDMAOLYARAGHSLDMLDCRRGQPCGPEFTTIF 180
OY 121 EHAALFLALGRPPAPPGFMPSPTFDMAOLYARAGHSLDMLDCRRGQPCGPEFTTIF 180
    |||||||
DB 121 EHAALFLALGRPPAPPGFMPSPTFDMAOLYARAGHSLDMLDCRRGQPCGPEFTTIF 180
OY 181 TRMGKCYTFNSGADGAEILLTTTRGGMNGDMLDVOOEYLPVWRDNEETPREVGIRVO 240
    |||||||
DB 181 TRMGKCYTFNSGADGAEILLTTTRGGMNGDMLDVOOEYLPVWRDNEETPREVGIRVO 240
OY 241 IHSQEBPIIIDQGLGVSPGYOTFVSCQOQOQLSFLPPMGDCSSASLNRYEPEPSDPLG 300
    |||||||
DB 241 IHSQEBPIIIDQGLGVSPGYOTFVSCQOQOQLSFLPPMGDCSSASLNRYEPEPSDPLG 300
OY 301 SPSPSPPTTLMGCRCLACETRIVYARKCGCRMVYMGDVPVCSPOQYKNCAPHAIDAMLR 360
    |||||||
DB 301 SPSPSPPTTLMGCRCLACETRIVYARKCGCRMVYMGDVPVCSPOQYKNCAPHAIDAMLR 360
OY 361 KDCSCAPNCASTRYAKELSMVRIPSRARFLARKLNRESEAYIAENVLADLFFFEALN 420
    |||||||
DB 361 KDCSCAPNCASTRYAKELSMVRIPSRARFLARKLNRESEAYIAENVLADLFFFEALN 420
OY 421 EYVEOKKAYEMSELLDGGOMGLFSGASLTLTLEILDYLCVEFRDKVLGYFWMRQHSQ 480
    |||||||
DB 421 EYVEOKKAYEMSELLDGGOMGLFSGASLTLTLEILDYLCVEFRDKVLGYFWMRQHSQ 480
OY 481 HSTNTNLQEGLSHRTQVPHLSLGR-----PP-----TPCAVTKTLSASHRT 524

```

```

DB 481 HSTNTNLQEGLSHRTQVPHLSLGRSTLLCSEDLPLVPVSPRSLSPPTAPATLSSSRP 540
    |||||||
OY 525 CYLV 528
    ||
DB 541 AVCV 544

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RESULT 5

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OY 090HC4 PRELIMINARY: PRT; 543 AA.
AC 090HC4;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE ACID SENSING ION CHANNEL 3 SPLICE VARIANT B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Renard S., Besnard F., Partiseti M., Graham D.;
RT ASIC3b a new modulatory subunit of the acid sensing ion channel
RT family ";
RL Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF195024; AAF19817.1; -
DR InterPro: IPR001873; ASC.
DR Pfam: PF00858; ASC; 1.
DR PRINTS: PRO1078; AMINACHANNEL.
SQ SEQUENCE 543 AA; 60331 MW; 9411BD1485BA93F1 CRC64;

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Query Match 91.1%; Score 2598; DB 4; Length 543;

Best Local Similarity 93.9%; Pred. No. 5,5e+230; Matches 491; Conservative 4; Mismatches 12; Indels 16; Gaps 3;

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OY 1 MKPTSGPEEARROPSDIRVFASNCNMHGLGHVFGPSLSLRGMMAAAVLSVATFLYOV 60
    |||||||
DB 1 MKPTSGPEEARROPSDIRVFASNCNMHGLGHVFGPSLSLRGMMAAAVLSVATFLYOV 60
OY 61 AERVRYRREHHQTALDERESHRLVFPAYTLNINPLRSRLPNLHMAGSALLGLDPA 120
    |||||||
DB 61 AERVRYRREHHQTALDERESHRLVFPAYTLNINPLRSRLPNLHMAGSALLGLDPA 120
OY 121 EHAALFLALGRPPAPPGFMPSPTFDMAOLYARAGHSLDMLDCRRGQPCGPEFTTIF 180
    |||||||
DB 121 EHAALFLALGRPPAPPGFMPSPTFDMAOLYARAGHSLDMLDCRRGQPCGPEFTTIF 180
OY 181 TRMGKCYTFNSGADGAEILLTTTRGGMNGDMLDVOOEYLPVWRDNEETPREVGIRVO 240
    |||||||
DB 181 TRMGKCYTFNSGADGAEILLTTTRGGMNGDMLDVOOEYLPVWRDNEETPREVGIRVO 240
OY 241 IHSQEBPIIIDQGLGVSPGYOTFVSCQOQOQLSFLPPMGDCSSASLNRYEPEPSDPLG 300
    |||||||
DB 241 IHSQEBPIIIDQGLGVSPGYOTFVSCQOQOQLSFLPPMGDCSSASLNRYEPEPSDPLG 300
OY 301 SPSPSPPTTLMGCRCLACETRIVYARKCGCRMVYMGDVPVCSPOQYKNCAPHAIDAMLR 360
    |||||||
DB 301 SPSPSPPTTLMGCRCLACETRIVYARKCGCRMVYMGDVPVCSPOQYKNCAPHAIDAMLR 360
OY 361 KDCSCAPNCASTRYAKELSMVRIPSRARFLARKLNRESEAYIAENVLADLFFFEALN 420
    |||||||
DB 361 KDCSCAPNCASTRYAKELSMVRIPSRARFLARKLNRESEAYIAENVLADLFFFEALN 420
OY 421 EYVEOKKAYEMSELLDGGOMGLFSGASLTLTLEILDYLCVEFRDKVLGYFWMRQHSQ 480
    |||||||
DB 421 EYVEOKKAYEMSELLDGGOMGLFSGASLTLTLEILDYLCVEFRDKVLGYFWMRQHSQ 480
OY 481 HSTNTNLQEGLSHRTQV---PHL-----SLGPP 507
    |||||||
DB 481 HSTNTNLQEGLSHRTQV---PHL-----SLGPP 507

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RESULT 6
ID 035240 PRELIMINARY; PRT; 533 AA.
AC 035240;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE PROTON GATED CATION CHANNEL DRASIC.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97407870; PubMed=9261094;
RA Wiedemann R., Bassilana F., de Welle J., Champigny G., Heurteaux C., Lazdunski M.;
RT "Molecular cloning of a non-inactivating proton-gated Na⁺ channel
specific for sensory neurons."
RL J. Biol. Chem. 272:20975-20978(1997).
DR EMBL; AF013598; AAB69328.1;
DR InterPro; IPR001873; ASC.
DR Pfam; PF00858; ASC.1.
SQ SEQUENCE 533 AA; 59226 MW; 294B57322C74B3DC CRC64;
Query Match 49.8% Score 2447; DB 11; Length 533;
Best Local Similarity 48.5%; Pred. No. 4e-216;
Matches 445; Conservative 49; Mismatches 37; Indels 2; Gaps 2;
QY 1 MKPTSGPEEA-RROPSDTRVFAASNGMGLHVGPGSLSLRGMMAAAYLVATFLYQ 59
DB 1 MKPRGLEEARROASDTRVFAASCTMGLHIFGPGGLTLRGRIMAVATLVLSLAFLYQ 60
QY 60 VAERARYREFHQTALDERESHRLVPAYVLCININPLRKRSLTPNDLHMAGSALLGDP 119
DB 61 VAERARYGEEHHTKTLDERESHQTLFPAYVLCININPLRKRSLTPNDLHMAGTALLGDP 120
QY 120 AEHAFLRALGRPARPGFMSPPTDMAOLYARAGHSLDMLDCRFRGOCGPEPNTT 179
DB 121 AEHAAYLALGQPARPGFMSPPTDMAOLYARAGHSLDMLDCRYRGOCGPEPNTVI 180
QY 180 FTRNGKCTFFNSGADGALLTTTRGGMGNGLDIMLDVQOEYLPRVNRNETPEVGRV 239
DB 181 FTRNGQCTFFNSGAGALLTTTRGGAGNGLEIMLDVQOEYLPRVNRNETPEVGRV 240
QY 240 QIHSEBEPITDOLGLGVSFGYOTFVSCQOQOQLSFLPPMGDCSSALNP-NYEPEDP 298
DB 241 QIHSDDEPRLDQLGFGARPGHQTFFVSCQOQOQLSFLPPMGDCNTASLDPPDFEPEDP 300
QY 299 LGSPPSPSPPYTLMGCLACETRYVARKCGRMVMPGDVPCSPQOYKNCAPALDAI 358
DB 301 LGSPPSPSPPYTLGCLACETRYVARKCGRMVMPGNSPVCSPQOYKNCAPALDAM 360
QY 359 LKRSQACPNCASTRYAKELSMVRIPSRARAFARKLNSEAYIAENVLALDIEFAL 418
DB 361 LKRDTCVPCNCASTRYAKELSMVRIPSRARAFARKLNSEAYIAENVLALDIEFAL 420
QY 419 NYETVEOKKAYEMSELDDIGOMGLFGASLLTLEILDYCEVFRKVLGYFMNRQHS 478
DB 421 NYEAVEOKKAAEVESELDDIGOMGLFGASLLTLEILDYCEVFRKVLGYFMNRSA 480
QY 479 QHRSSTNLQEGLSHRTQVPHSLSGRPRTPCAVTKTSLASHRTCYLVOL 531
DB 481 QKRSQNTLQEGLSHRTQVPHSLSGRPRTPCAVTKTSLASHRTCYLVOL 533

RESULT 7
ID 0925H0 PRELIMINARY; PRT; 512 AA.
AC 0925H0;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE BRAIN SODIUM CHANNEL 1 ALPHA SUBUNIT.
GN ACCN1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RX MEDLINE=97188490; PubMed=9037075;
RA Garcia-Anoveros J., Deffler B., Neville-Golden J., Hyman B.T., Corey D.P.;
RT "Bnac1 and Bnac2 constitute a new family of human neuronal sodium channels related to degenerins and epithelial sodium channels."
RL Proc. Natl. Acad. Sci. U.S.A. 94:1459-1464(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RX MEDLINE=21204130; PubMed=11306621;
RA Garcia-Anoveros J., Samad T.A., Zuvela-Jelaska L., Woolf C.J., Corey D.P.;
RT "Transport and Localization of the DEG/ENAC Ion Channel Bnac1alpha to Peripheral Mechanosensory Terminals of Dorsal Root Ganglia Neurons."
RL J. Neurosci. 21:2678-2686(2001).
DR EMBL; AF348465; AAK40101.1;
KW Ionic channel.
SQ SEQUENCE 512 AA; 57739 MW; 7D81A77C3B347B04 CRC64;
Query Match 47.9% Score 1367; DB 11; Length 512;
Best Local Similarity 50.6%; Pred. No. 6.3e-117;
Matches 255; Conservative 83; Mismatches 140; Indels 26; Gaps 5;
QY 7 PEARROPSDTRVFAASNGMGLHVGPGSLSLRGMMAAAYLVATFLYQYAEVRY 66
DB 7 PSESLDQSSIQIFANSTLHGIRHIFVYGLTIRVLMVAFAVGSGLLVESSEVSY 66
QY 67 YREFHQTALDERESHRLVPAYVLCININPLRKRSLTPNDLHMAGSALLGID-----PAE 121
DB 67 YESVOHYKQDEVAQSLVPAYVLCININPLRKRSLTPNDLHMAGSALLGID-----PAE 126
QY 122 HAA---FLRALGRPARPGFMSPPTDMAOLYARAGHSLDMLDCRFRGOCGPEPNTT 178
DB 127 HLAQPTVLEALRQANRKHNYK-QFSMLEPLHAYGHDLDMLYCFKQEGCHQDFTT 185
QY 179 IFTRMGKCTFFNSGADGALLTTTRGGMGNGLDIMLDVQOEYLPRVNRNETPEVGRV 238
DB 186 VFTKYGKCYMNSGDEGKPLTTVKGNGLEIMLDIQOEXYLPINGETETFEAGVK 245
QY 239 VOHSQEBEPITDOLGLGVSFGYOTFVSCQOQOQLSFLPPMGDCSSALNPNYEPEDP 298
DB 246 VOHSQEBEPITDOLGLGVSFGYOTFVSCQOQOQLSFLPPMGDCSSALNPNYEPEDP 298
QY 299 LGSPPSPSPPYTLMGCLACETRYVARKCGRMVMPGDVPCSPQOYKNCAPALDAI 358
DB 299 -----FPYSTITACRIDCETRYIYENCNCRVMPHMGDAPCTPQHKECAPALGL 350
QY 359 LKQDS--CACPNCASTRYAKELSMVRIPSRARAFARKLNSEAYIAENVLALDIEFE 416
DB 351 AEKDSNVCCLCTPCNLIRYNKELSMVRIPSRARAFARKLNSEAYIAENVLALDIEFE 410
QY 417 ALNTEYEQKAYEMSELDDIGOMGLFGASLLTLEILDYCEVFRKVLGYFMNRQ 476
DB 411 ALNTEYEQKAYEMSELDDIGOMGLFGASLLTLEILDYCEVFRKVLGYFMNRQ 470
QY 477 HSRHSSTNLQEGLSHRTQVPH 500
DB 471 EESGHENMSTCDTPMNHSETISH 494

RESULT 8
ID 088762 PRELIMINARY; PRT; 513 AA.
AC 088762;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)


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DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE ASIC-BETA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98374336; PubMed=9707631;
RA Chen C.C., England S., Akopian A.N., Wood J.N.;
RT "A sensory neuron-specific, proton-gated ion channel."
RL Proc. Natl. Acad. Sci. U.S.A. 95:10240-10245(1998).
CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNELS
CC FAMILY.
DR EMBL: AJ006519; CAA07080.1;
DR InterPro: IPR001873; ASC.
DR Pfam: PF00858; ASC. 2.
DR PROSITE: PS01206; ASC. 1.
KW Glycoprotein; Ion transport; Ionic channel; Transmembrane.
SQ SEQUENCE 513 AA; 57016 MW; 02100E166E2F32A3 CRC64;

Query Match 47.0%; Score 1340; DB 11; Length 513;
Best Local Similarity 49.8%; Pred. No. 1.9e-114;
Matches 256; Conservative 83; Mismatches 141; Indels 34; Gaps 7;

QY 1 MKPTSGPEEARROPSDIRVFASNCNMHGLGHVGPGLSLRRGMAAAVYLSVATPLYOV 60
   1 MEAGSELDEGDDSPDLVAFANSCTLHGASHVEEGPGPROMLVAVFIALGAFLCQY 60
DB 1
QY 61 AERVRYREPHHOTALDERESHRLVPAVYTCINPLRGRSLPNDLHWAGSALLGDPA 120
   61 GDRVAYILSPHYTLDEVAITSELVPAVYFCNTNVRLSQLSYPLDLYL-APMLGDES 119
DB 121 EHAFLRALGRPPAPPGFMPSPFDMAOLYARAGHSLDMLDLCRFRGQCGPENFTTIF 180
   120 DDGCVPLA---PPGEAFSGEP-FNLHRYNRSCHRLDMLYLCVCGCGCPHNSVVF 175
DB 120
QY 181 TRMGKCYTFNSGADGAEELLTTRGCMGNGIDMLDVOQEEYLLVWRDNEETPREVGIRVQ 240
   176 TRYKCYTFNSGDDGRPRILTKMGGTGNGLEIMLDIOQDEYLLPWGGETDSTFEAGIKVQ 235
DB 176
QY 241 IHSQDEPPIIDOLGLGVSPGYQTFVSCQOQOQLFLPRPMWDCSSASLNPVYEEPPSPDLG 300
   236 IHSQDEPPIIDOLGLGVAPGFQTFVSCQEQRLYLPSPMGTCAVYMDSDF----- 286
DB 236
QY 301 SPSPSPSPPTTLMGCRCLACTRYVARKGCRMYMPGDVYVCSPOOYKNCAPDAIDAILR 360
   287 -----FDSYSTACRIDCETRYLVENCNCRMYHMPGDAPYCTPEOYKECADPALDFLVE 340
DB 287
QY 361 KDS--CACPNPCASTRYAKELSWRIPSRARFLARKLRSEAYIAENVLADIFFEAL 418
   341 KDQCYCVCEMPCMLTRYGKELSMVKIPSKASAKYLAKEFKSEQYIGENLVLDIFFEVL 400
DB 341
QY 419 NYETVEQKRAYEMSELLDIDIGOMGLFICASLTLIEILDYLCVFRDKYLGYFMNRQHS 478
   401 NYETIEQKRAYETIAGLDIGOMGLFICASILTVELFPIYAEVYIKHRLC-----RRGKC 456
DB 401
QY 479 QRHSSTNLQEGLSHRTQVPHLSLGRPPPTPPC 512
   457 QKEAKRSSADKGYA-----LSLDVYKRNHNC 482
DB 457

RESULT 9
091YB8 PRELIMINARY; PRT; 559 AA.
AC 091YB8;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE ION CHANNEL.

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GN ASIC 1B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX Baesler E.L., Ngo-Anh J., Geisler H.S., Ruppersberg J.P., Grunder S.;
RT "Molecular and functional characterization of acid-sensing ion channel
   (ASIC) 1b."
RL J. Biol. Chem. 276:33783-33787(2001).
DR EMBL: AJ309926; CAC44267.1;
SQ SEQUENCE 559 AA; 62217 MW; 0F438117B95C18E5 CRC64;

Query Match 47.0%; Score 1339; DB 11; Length 559;
Best Local Similarity 49.8%; Pred. No. 2.7e-114;
Matches 256; Conservative 83; Mismatches 141; Indels 34; Gaps 7;

QY 1 MKPTSGPEEARROPSDIRVFASNCNMHGLGHVGPGLSLRRGMAAAVYLSVATPLYOV 60
   47 MEAGSELDEGDDSPDLVAFANSCTLHGASHVEEGPGPROMLVAVFIALGAFLCQY 106
DB 47
QY 61 AERVRYREPHHOTALDERESHRLVPAVYTCINPLRGRSLPNDLHWAGSALLGDPA 120
   107 GDRVAYILSPHYTLDEVAITSELVPAVYFCNTNVRLSQLSYPLDLYL-APMLGDES 165
DB 107
QY 121 EHAFLRALGRPPAPPGFMPSPFDMAOLYARAGHSLDMLDLCRFRGQCGPENFTTIF 180
   166 DDGCVPLA---PPGEAFSGEP-FNLHRYNRSCHRLDMLYLCVCGCGCPHNSVVF 221
DB 166
QY 181 TRMGKCYTFNSGADGAEELLTTRGCMGNGIDMLDVOQEEYLLVWRDNEETPREVGIRVQ 240
   222 TRYKCYTFNSGDDGRPRILTKMGGTGNGLEIMLDIOQDEYLLPWGGETDSTFEAGIKVQ 281
DB 222
QY 241 IHSQDEPPIIDOLGLGVSPGYQTFVSCQOQOQLFLPRPMWDCSSASLNPVYEEPPSPDLG 300
   282 IHSQDEPPIIDOLGLGVAPGFQTFVSCQEQRLYLPSPMGTCAVYMDSDF----- 332
DB 282
QY 301 SPSPSPSPPTTLMGCRCLACTRYVARKGCRMYMPGDVYVCSPOOYKNCAPDAIDAILR 360
   333 -----FDSYSTACRIDCETRYLVENCNCRMYHMPGDAPYCTPEOYKECADPALDFLVE 386
DB 333
QY 361 KDS--CACPNPCASTRYAKELSWRIPSRARFLARKLRSEAYIAENVLADIFFEAL 418
   387 KDQCYCVCEMPCMLTRYGKELSMVKIPSKASAKYLAKEFKSEQYIGENLVLDIFFEVL 446
DB 387
QY 419 NYETVEQKRAYEMSELLDIDIGOMGLFICASLTLIEILDYLCVFRDKYLGYFMNRQHS 478
   447 NYETIEQKRAYETIAGLDIGOMGLFICASILTVELFPIYAEVYIKHRLC-----RRGKC 502
DB 447
QY 479 QRHSSTNLQEGLSHRTQVPHLSLGRPPPTPPC 512
   503 QKEAKRSSADKGYA-----LSLDVYKRNHNC 528
DB 503

RESULT 10
055163 PRELIMINARY; PRT; 563 AA.
AC 055163;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE PROTON-GATED CATION CHANNELS MODULATOR SUBUNIT MDEG2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MISTAR; TISSUE=BRAIN;
MEDLINE=98037807; PubMed=9368048;
Linguegla E., Demelille E., Bassilana F., Heurteaux C., Sakai H.,

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RA Waldmann R., Lazdunski M.;
RT "A modulatory subunit of acid sensing ion channels in brain and dorsal
RT root ganglion cells.";
RL J. Biol. Chem. 272:29778-29783(1997).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNELS
CC FAMILY.
DR EMBL: Y14635; CAA74979.1; -.
DR InterPro: IPR001873; ASC.
DR Pfam: PF00858; ASC. 1.
DR PROSITE: PS01206; ASC. 1.
KW Glycoprotein; Ion transport; Ionic channel; Transmembrane.
SQ SEQUENCE 563 AA: 63115 MW; DCE1BA0A45F21E2 CRC64;

Query Match 43.8%; Score 1249.5; DB 11; Length 563;
Best Local Similarity 47.5%; Pred. No. 4.5e-106;
Matches 245; Conservative 79; Mismatches 151; Indels 41; Gaps 8;

OY 6 GPEEAR-OPSDIRVFASNCMHGLGHV---FGPGSLSLRGMAAAVVLVSATFLYOV 60
DB 50 GGVARRGRPS-----LSRTKLHGLRHMCAGRTAAGSFORRALVWLAFCTSLGLLSMS 104
OY 61 AERVYTYEENHQTALDERESHRLVPRAVTLGNINPLRSRLTPNDLMAGSALLGDPA 120
DB 105 SNRLLYWLSPSHYVHREWSKQLPFPAYVCNNPLRFPRLSKDLYYAAGHWGLLPLN 164
OY 121 EHA-AFLRALGRPPAPG-----FMSPFED--MAQLYRAGHSLDMLDCRF 166
DB 165 RPARLVSELRLGDEPRRQWFKLADFLPLRPRHFEBSAFAFMRLCHOLEDMLSCKY 224
OY 167 RGQPCGPNFTTIFTRMGKCYTFNSGADGAELELTTRGGMGNDLMDVQOEEYLPWR 226
DB 225 RQELGPHNFSSVFYKCYMFNSGEDGKPLLTIVKGTGNGLEIMDIOODEYLPWG 284
OY 227 DNEETPFEVGIRVOYHSGOEPPIIDOLGIVSPGYOTFVSCQOQLSFLPPMGSCSSAS 286
DB 285 ETEETTFEAGVAVOIHSGOEPPIIDOLGIVSPGYOTFVSCQOQLSFLPPMGSCSSAS 344
OY 287 LNPNPEPSDPLGSPSPSPRYTLMGCRACETRIVYARKGCRHVMYPGDVPYCSPOQ 346
DB 345 MGLDF-----FPVYSITACRIDCETRIYVENCNCVMHMPGAPRCPTEQ 389
OY 347 YKNCARPAIDALRKDS--CACPNPCASTRYAKELSMYRIPSRARARLAKLNSEAYI 404
DB 390 HKECAEPALGLAEKDSNYCLCTPCNLTIRYKELSMYKIPSTAKLEKFNSEKI 449
OY 405 AENVALLDIFFEALNYETVEOKKAYEMSELGDIGOGMLFGASLITLLEIDYLCVF 464
DB 450 SENILYLDIFFEALNYETVEOKKAYEVALADIGOGMLFGASLITLLEIDYIYELI 509
OY 465 RDKVLGYFWNRHOSQHSSTNLDEGLSHRTQVPH 500
DB 510 KEKLLDLGKEEBSGSHDENMSTCDTMNHSSETISH 545

RESULT 11
061203 PRELIMINARY; PRT; 563 AA.
AC 061203;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE PROTON-GATED CATION CHANNELS MODULATORY SUBUNIT MEG2 (AMILORIDE-
DE SENSITIVE CATION CHANNEL 1, NEURONAL) (DEGENERIN) (SODIUM CHANNEL 1).
GN ACCN1 OR MBNAC1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE-BRAIN;
RX MEDLINE=98037807; Pubmed=9368048;

RA Lingueglia E., Deweille E., Bassilana F., Heurteaux C., Sakai H.,
RA Waldmann R., Lazdunski M.;
RT "A modulatory subunit of acid sensing ion channels in brain and dorsal
RT root ganglion cells.";
RL J. Biol. Chem. 272:29778-29783(1997).
CC (2)
RN SEQUENCE OF 335-538 FROM N.A.
RP TISSUE-BRAIN;
RC MEDLINE=97188490; Pubmed=9037075;
RX Garcia-Anoveros J., Derfler B., Neville-Golden J., Hyman B.T.,
RA Corey D.P.;
RT "BNC1 and BNC2 constitute a new family of human neuronal sodium
RT channels related to degenerins and epithelial sodium channels.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:1459-1464(1997).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNELS
CC FAMILY.
DR EMBL: Y14634; CAA74978.1; -.
DR MGD: U57353; AAB49183.1; -.
DR InterPro: IPR001873; ASC.
DR Pfam: PF00858; ASC. 1.
DR PRINTS: PR01078; AMINACHANNEL.
DR PROSITE: PS01206; ASC. 1.
KW Glycoprotein; Ion transport; Ionic channel; Transmembrane.
SQ SEQUENCE 563 AA: 63204 MW; 56F7BA0A214BA39 CRC64;

Query Match 43.8%; Score 1247.5; DB 11; Length 563;
Best Local Similarity 47.3%; Pred. No. 6.8e-106;
Matches 244; Conservative 80; Mismatches 151; Indels 41; Gaps 8;

OY 6 GPEEAR-OPSDIRVFASNCMHGLGHV---FGPGSLSLRGMAAAVVLVSATFLYOV 60
DB 50 GGVARRGRPS-----LSRTKLHGLRHMCAGRTAAGSFORRALVWLAFCTSLGLLSMS 104
OY 61 AERVYTYEENHQTALDERESHRLVPRAVTLGNINPLRSRLTPNDLMAGSALLGDPA 120
DB 105 SNRLLYWLSPSHYVHREWSKQLPFPAYVCNNPLRFPRLSKDLYYAAGHWGLLPLN 164
OY 121 EHA-AFLRALGRPPAPG-----FMSPFED--MAQLYRAGHSLDMLDCRF 166
DB 165 RPARLVSELRLGDEPRRQWFKLADFLPLRPRHFEBSAFAFMRLCHOLEDMLSCKY 224
OY 167 RGQPCGPNFTTIFTRMGKCYTFNSGADGAELELTTRGGMGNDLMDVQOEEYLPWR 226
DB 225 RQELGPHNFSSVFYKCYMFNSGEDGKPLLTIVKGTGNGLEIMDIOODEYLPWG 284
OY 227 DNEETPFEVGIRVOYHSGOEPPIIDOLGIVSPGYOTFVSCQOQLSFLPPMGSCSSAS 286
DB 285 ETEETTFEAGVAVOIHSGOEPPIIDOLGIVSPGYOTFVSCQOQLSFLPPMGSCSSAS 344
OY 287 LNPNPEPSDPLGSPSPSPRYTLMGCRACETRIVYARKGCRHVMYPGDVPYCSPOQ 346
DB 345 MGLDF-----FPVYSITACRIDCETRIYVENCNCVMHMPGAPRCPTEQ 389
OY 347 YKNCARPAIDALRKDS--CACPNPCASTRYAKELSMYRIPSRARARLAKLNSEAYI 404
DB 390 HKECAEPALGLAEKDSNYCLCTPCNLTIRYKELSMYKIPSTAKLEKFNSEKI 449
OY 405 AENVALLDIFFEALNYETVEOKKAYEMSELGDIGOGMLFGASLITLLEIDYLCVF 464
DB 450 SENILYLDIFFEALNYETVEOKKAYEVALADIGOGMLFGASLITLLEIDYIYELI 509
OY 465 RDKVLGYFWNRHOSQHSSTNLDEGLSHRTQVPH 500
DB 510 KEKLLDLGKEEBSGSHDENMSTCDTMNHSSETISH 545

RESULT 12
09NOA4 PRELIMINARY; PRT; 539 AA.
ID 09NOA4;
AC 09NOA4;
DT 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE PUTATIVE ACID-SENSING ION CHANNEL (ACID SENSING ION CHANNEL 4).
 GN ASIC4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=PUTITARY;
 RX MEDLINE=20309050; PubMed=10852210;
 RA Grunder S., Geisler H.S., Baessler E.L., Ruppersberg J.P.;
 RT "A new member of acid-sensing ion channels from pituitary gland.";
 RL Neuroreport 11:1607-1611(2000).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21453362; PubMed=1571555;
 RA Grunder S., Geisler H.S., Rainier S., Fink J.K.;
 RT "Acid-sensing ion channel (ASIC) 4 gene: physical mapping, genomic
 RT organisation, and evaluation as a candidate for paroxysmal dystonia.";
 RL Eur. J. Hum. Genet. 9:672-676(2001).
 DR EMBL: AJ271643; CAB93980.1; -;
 DR EMBL: AJ408881; CAC51338.1; -;
 DR EMBL: AJ408882; CAC51338.1; JOINED.
 DR EMBL: AJ408883; CAC51338.1; JOINED.
 DR EMBL: AJ408884; CAC51338.1; JOINED.
 DR InterPro: IPR001873; ASC.
 DR Pfam: PF00858; ASC; 2.
 DR PRINTS: PRO1078; AMINACHANNEL.
 SQ SEQUENCE 539 AA; 59206 MW; 9C7ACF0DF5EC17E9 CRC64;

Query Match 41.4%; Score 1180; DB 4; Length 539;
 Best Local Similarity 49.8%; Pred. No. 1e-99;
 Matches 247; Conservative 58; Mismatches 161; Indels 30; Gaps 9;

QY 14 PSIRVPAASCSMHGIVFGPSLSLRGMAAAVYLSVATFLYQVAERVRYREHHQ 73
 DB 39 PRDIAFASTSTLHGIRACGPGPHGRLRTLMALTLTSLAFLYQAGLARGTLRPHL 98
 QY 74 TALDERSHLV-FPAVTLGNIPLRSLRTPNDL-HWAGSALLGLDPAEHAFLRALGR 131
 DB 99 VANDPAPAPAVAGFPATVLCINIRFRHSALSDADIFHLAN--LTGLRPKDRDGRAGLR 156
 QY 132 PPAAPGFPSPPTDMAOLYARAGSHLDDMLDCRFQPCGPPENFTTIFRMKCYTENS 191
 DB 157 YPEP-----DMDVILNRTGHQDLADMLKSCNFGHSCASNFVYTRRYGKCYTFN- 206
 QY 192 GAGCAELLTTTRGCMGNDIMLDVQOEELTPWRDNEFPFEVGIIVQIHSGEPPYID 251
 DB 207 -ADPRSSLPRAGMGSGLEIMLDIOEEYLPWRETNETSFEGIVQIHSGEPPYIH 265
 QY 252 QLGIVGSPGVOTFVSCQOOLSFLLPPMGDCSSASLNPNTEPEPSDPLGSPSPSPYT 311
 DB 266 QLGIVGSPGVOTFVSCQOOLTYLPQPMGNCRAES-----ELREPELQGYAYS 314
 QY 312 LMGRCLACETRYVARKCGCRMYVPGDVPVCSPOQYKNCAPDAIDAI--LRKSCACPNP 369
 DB 315 VSACRLRCEKEAVLQRCHEMVMHPNETICPPNIYIECADHTLDSGGGEGECPCPTP 374
 QY 370 CASRRAKELSMVRIIPRSARARFLARKINSEAVIAENVIALDIFFEALNTEYQOKAY 429
 DB 375 CNLIRGKEISWRIIPRGSARRYLARKYNNREYIYRENFLVDVFEALTSSEAEQORAY 434
 QY 430 EMSLELDIGGOMGLFGASLTLTLEILDYLCIEVFRDKVLGYEWNROHSQHSSTNLQOE 489
 DB 435 GLSALDGLDGGOMGLFGASLTLTLEILDYLYEVSWDR-LKRVARRKPTPLRTSTGIST 493
 QY 490 -GLGSARTQVPHSLG 504
 DB 494 LGLQELKEQSPCSLIG 509

RESULT 13
 ID Q9JHS6 PRELIMINARY; PRT; 539 AA.
 AC Q9JHS6;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
 DE PUTATIVE ACID-SENSING ION CHANNEL.
 GN ASIC4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX MEDLINE=20309050; PubMed=10852210;
 RA Grunder S., Geisler H.S., Baessler E.L., Ruppersberg J.P.;
 RT "A new member of acid-sensing ion channels from pituitary gland.";
 RL Neuroreport 11:1607-1611(2000).
 DR EMBL: AJ271642; CAB93984.1; -;
 DR InterPro: IPR001873; ASC.
 DR Pfam: PF00858; ASC; 2.
 DR PRINTS: PRO1078; AMINACHANNEL.
 SQ SEQUENCE 539 AA; 59324 MW; 3D73DE0EAEFF7097 CRC64;

Query Match 41.0%; Score 1169; DB 11; Length 539;
 Best Local Similarity 48.7%; Pred. No. 1e-98;
 Matches 243; Conservative 60; Mismatches 166; Indels 30; Gaps 9;

QY 6 GPEARQPSDIRVPAASCSMHGIVFGPSLSLRGMAAAVYLSVATFLYQVAERVR 65
 DB 31 GAAGPAPAPDLATFASTSTLHGIRACGPGPHGRLRTLMALTLTSLAFLYQAGLARGTLRPHL 90
 QY 66 YRFEFHQIALDERESHRLV-FPAVTLGNIPLRSLRTPNDL-HWAGSALLGLDPAEHA 123
 DB 91 GYLRLPHLVANDPAPAPAVAGFPATVLCINIRFRHSALSDADIFHLAN--LTGLRPKDRD 148
 QY 124 AFLRALRPPAPGFPSPPTDMAOLYARAGSHLDDMLDCRFQPCGPPENFTTIFRM 183
 DB 149 GHRAAGLRPEP-----DMDVILNRTGHQDLADMLKSCNFGHSCASNFVYTRY 199
 QY 184 GKCTFNSGADGALLTTTRGCMGNDIMLDVQOEELTPWRDNEFPFEVGIIVQIHSGEPPYID 243
 DB 200 GKCTFEN--ADPOSSLPRAGMGSGLEIMLDIOEEYLPWRETNETSFEGIVQIHSGEPPYIH 257
 QY 244 QEEPPYIDQLGIVGSPGVOTFVSCQOOLSFLLPPMGDCSSASLNPNTEPEPSDPLGSPS 303
 DB 258 QEEPPYIHQLGIVGSPGVOTFVSCQOOLTYLPQPMGNCRAES-----KLREPE 306
 QY 304 PPSPPYTLMGCRCLACETRYVARKCGCRMYVPGDVPVCSPOQYKNCAPDAIDAI--LRK 361
 DB 307 LOGTSAYSVSACRLRCEKEAVLQRCHEMVMHPNETICPPNIYIECADHTLDSGGGSE 366
 QY 362 DSCACPNPCASSTRYAKELSMVRIIPRSARARFLARKINSEAVIAENVIALDIFFEALNTE 421
 DB 367 GPCCFPPTCNLIRGKEISWRIIPRGSARRYLARKYNNREYIYRENFLVDVFEALTSSE 426
 QY 422 TVEOKKAYEMSELGADIGGOMGLFGASLTLTLEILDYLCIEVFRDKVLGYEWNROHSQORH 481
 DB 427 AMEARAAYGLSALLDGGOMGLFGASLTLTLEILDYLYEVSWDR-LKRVARRKPTPLR 485
 QY 482 SSTNLQOE-GLGSARTQV 499
 DB 486 TSTGISTLGLQELKEQSP 504

RESULT 14
 ID Q9QYV9 PRELIMINARY; PRT; 539 AA.
 AC Q9QYV9;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, last sequence update)

01-JUN-2001 (Tremblrel. 17, last annotation update)
DE SPASIC PROTEIN.
GN SPASIC.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN
[1]
RN
SEQUENCE FROM N.A.
RA Akopian A.N., England S., Chen C.C., Wood J.N.;
RT "A non-inactivating proton-gated ion channel is broadly expressed in
the central nervous system."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ242534; CAB61836.1; -
DR InterPro; IPR001873; ASC.
DR Pfam; PF00858; ASC; 2.
DR PRINTS; PRO1078; AMINACHANNEL.
SQ SEQUENCE 539 AA; 59352 MW; 2DE4838AA0547097 CRC64;

Query Match 40.9%; Score 1167; DB 11; Length 539;
Best Local Similarity 48.5%; Pred. No. 1.6e-98;
Matches 242; Conservative 61; Mismatches 166; Indels 30; Gaps 9;

QY 6 GPEEARQPSDTRVFNASHGNGHVGPGSLSRGGMMAAVVSVATFLYOVAERVY 65
DB 31 GAAQPPAARDLATFASSTLHGLGRACGPGHGLRTLWVLAFLTSLAFLYQAASLAR 90
QY 66 YRREFHQTALDERESHRLV-FPAVTLNINPLRRSLTPNDL-HWAGSALGLDPAEHA 123
DB 91 GYLTRPHLVADPAPAPVAGFPATVLCNINFRHSALSDADIFILAN-LTGLPRKQND 148
QY 124 AFLRALGRPPAPGFPSPFTFDMALYARAGHSLDMLDCRFRCQPCGPFENFTTFTRM 183
DB 149 GHRAAGLYRPEP-----DMVDILNRTGHQLADMLKSCNFSGHCSASNFVYTRY 199
QY 184 GKCYFNSGADAEALLTTRGGMGNGLDIMLVQOEYLPVRDNEETPREVGIVQHS 243
DB 200 GKCYFN--ADPOSLPSRAGSGGLEMLDIOEETPLRKRENETSFEAGIVQHS 257
QY 244 QEEPRIIDGLGVSQYQTFVSCQOOLSFLLPPWGDCCSSALNPNYEPSPDPLGSPS 303
DB 258 QEEPRYIHLGFGVSPGQTFVSCQOQLTYLPQWGNCRAS-----KLREPE 306
QY 304 PSPSPYTLGMCRLACETRYVARCKGCRMYVPGDYVCSPOQYKNCAPDAIDAI-LRK 361
DB 307 LOGYSAYSVSACRLCEKAEVLRCHCRMYHMPGNETTICPNYIECADHTLDSLGSE 366
QY 362 DSCACPNPCASTRYAKELSMVRIIPRAARFLARKLNSEAVIAENVLALDIEFEALNYE 421
DB 367 GPCFPTFCNLTTRYKEISMVAKIPRGSARVLAARYNNRETYIRENPLVDVFEALTSE 426
QY 422 TVEOKKAYEMSELLDGGOMGLFGASLLTLEILDYLCIEYFRDKVLGYEWNROHSORH 481
DB 427 AMEORAAYGLSLDGLDGGOMGLFGASILLTLEILDYIYEVSMWR-LKRVARRRKTPLR 485
QY 482 SSTNLDE-GLGSHTQYV 499
DB 486 TSTGISTLGLQELKEQSP 504

RESULT 15

096FT7 PRELIMINARY; PRT; 647 AA.
AC 096FT7;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:17248).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN, AND ANAPLASTIC OLIGODENDROGLIOMA WITH 1P/19Q LOSS;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010439; AAH10439.1; -
SQ SEQUENCE 647 AA; 70033 MW; 87333716882872D0 CRC64;

Query Match 39.7%; Score 1130.5; DB 4; Length 647;
Best Local Similarity 48.7%; Pred. No. 4.7e-95;
Matches 242; Conservative 53; Mismatches 151; Indels 51; Gaps 10;

QY 14 PSDIVFASNCMNGHVGPGSLSRGGMMAAVVSVATFLYOVAERVYEFHQQ 73
DB 166 PDLATFASSTLHGLGRACGPGHGLRTLWVLAFLTSLAFLYQAAGLAGYTLRPHL 225
QY 74 TADRESHRLV-FPAVTLNINPLRRSLTPNDL-HWAGSALGLDPAEHAFLALGR 131
DB 226 VAMDPAAPAPVAGFPATVLCNINFRHSALSDADIFILAN-LTGLPRKDRGHAAAGLR 283
QY 132 PPAPGFMPSPFTFDMALYARAGHSLDMLDCRFRCQPCGPFENFTTFTRMKCYTENS 191
DB 284 YPEP-----DMVDILNRTGHQLADMLKSCNFSGHCSASNFVYTRYGKCYTEN- 333
QY 192 GADGAEALLTTRGGMGNGLDIMLVQOEYLPVRDNEETPREVGIVQHSQEEPRIID 251
DB 334 -ADPSSSLPSRAGSGGLEMLDIOEETPLRKRENETSFEAGIVQHSQEEPRYIH 392
QY 252 QGLGVSPQYQTFVSCQOOLSFLLPPWGDCCSSALNPNYEPSPDPLGSPSPSPPYT 311
DB 393 QUGFVSGFQTFVSCQOQLRTYLPQWGNCRAS-----ELREPELGYSAYS 441
QY 312 LMGCLACETRYVARCKGCRMYVNP--GDYVCSPOQYKNCAPDAIDAILRKDSCACP 368
DB 442 VSACRLRCEKEAVLRCHCRMYHMPDLSLGGP-----EGPCFCPT 481
QY 369 PCASTRYAKELSMVRIIPRAARFLARKLNSEAVIAENVLALDIEFEALNYEIOEKA 428
DB 482 PCNLTTRYKEISMVRIIPRGSARVLAARYNNRETYIRENPLVDVFEALTSEAEQRAA 541
QY 429 YEMSELLDGGOMGLFGASLLTLEILDYLCIEYFRDKVLGYEWNROHSSTNLQ 488
DB 542 YGLSLDGLDGGOMGLFGASILLTLEILDYIYEVSMWR-LKRVARRRKTPLRSTGIS 600
QY 489 E-GLGSHTQYVPHSLG 504
DB 601 TLGLQELKEQSPSLG 617

Search completed: October 11, 2002, 07:26:20
Job time : 93 secs

Fri Oct 11 09:49:28 2002

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 11, 2002, 03:46:04 : Search time 65 seconds
(without alignments)
907.387 Million cell updates/sec

Title: US-09-530-233-2
Perfect score: 2851
Sequence: 1 MKPTSGPEBAROPSDIRVF.....CAVTKTLASHTCYLVTQI

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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- 19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2851	100.0	531	20	AA09509
2	2833	99.4	531	21	AA09181
3	2706	94.9	549	20	AAW8252
4	2598	91.1	543	20	AAW8250
5	2481	87.0	538	20	AAW8251
6	2447	85.8	533	19	AAW8508
7	2447	85.8	533	21	AAV69179
8	1365	47.9	512	19	AAW8506
9	1365	47.9	512	20	AAW93420
10	1365	47.9	512	21	AAV69177
11	1340	47.0	513	20	AAV03186

ALIGNMENTS

12	1337	46.9	559	19	AAW8507	Rat acid sensing 1
13	1337	46.9	559	21	AAV69178	A rat acid-sensit
14	1329	46.6	526	19	AAW8504	Rat acid sensing 1
15	1329	46.6	526	20	AAV03188	Rat Acid sensitive
16	1329	46.6	526	21	AAV69175	A rat acid-sensit
17	1319	46.3	514	19	AAW8505	Human acid sensing
18	1319	46.3	514	21	AAV69176	A partial acid-sen
19	1249.5	43.8	563	19	AAW8509	Rat acid sensing 1
20	1246.5	43.7	563	21	AAV69180	A rat acid-sensit
21	1180	41.4	539	19	AAW80318	Neurodegenerative
22	1180	41.4	539	22	AAE10857	Human brain sodium
23	1175	41.2	539	19	AAW80315	Neurodegenerative
24	1174	41.2	539	22	AAE10898	Human brain sodium
25	1170	41.0	539	21	AAV53870	Amino acid sequenc
26	1134.5	39.8	587	19	AAW80316	Neurodegenerative
27	806.5	28.3	401	21	AAW807750	A human acid sensi
28	616	21.6	505	22	AAV9115	Amino acid sequenc
29	614	21.5	505	22	AAV9118	Amino acid sequenc
30	613	21.5	505	22	AAV9116	Amino acid sequenc
31	613	21.5	505	22	AAV9117	Amino acid sequenc
32	532.5	18.7	319	20	AAV03187	Rat Acid sensitive
33	369.5	13.0	707	22	ABG24674	Novel human diagno
34	342.5	12.0	493	13	AAW20107	Mec-4 gene product
35	342.5	12.0	493	14	AAW33890	mec-4 protein. Ca
36	335.5	11.8	150	22	ABW16915	Human nervous syst
37	335.5	11.8	150	22	AAW42375	Human polypeptide
38	328	11.5	103	19	AAW80317	Neurodegenerative
39	326	11.4	508	14	AAW42747	deg-3 gene product
40	315.5	11.1	669	22	AAE10335	Human transporter
41	298.5	10.5	562	14	AAW42743	mec-4 gene product
42	254	8.9	294	13	AAW20106	deg-1 gene product
43	254	8.9	294	14	AAW33889	deg-1 protein. Ca
44	248.5	8.7	548	22	ABW58115	Drosophila melanog
45	247.5	8.7	516	22	ABW63689	Drosophila melanog

RESULT 1
ID AA09509 standard; Protein: 531 AA.
AC AA09509;
DT 16-JUL-1999 (first entry)
DE Human proton-gated cation channel.
KW Human: non-inactivating aniloride-sensitive proton-gated cation channel;
KW hASIC3; analgesic.
OS Homo sapiens.
XX MO0921981-AL
XX MO0921981-AL
XX 06-MAY-1999.
XX 29-OCT-1998; 98WO-CA01016.
XX 29-OCT-1997; 97CA-2219713.
XX (UYMC-) UNIV MCGILL.
XX Babinski K, Seguela P.
XX WPI: 1999-312958/26.
XX N-PSDB: AAX56237.
XX Use of human protein as a proton-gated cation channel
XX Claim 1; Fig 1; 32pp; English.

CC The present sequence is a human non-inactivating amiloride-sensitive
 CC proton-gated cation channel designated hASIC3. hASIC3, its encoding
 CC nucleic acid and the recombinant host cell are useful in a composition
 CC or a kit for screening compounds useful as proton-gated cation channel
 CC ligands. The ligands are useful as analgesics.

XX Sequence 531 AA;

Query Match 100.0%; Score 2851; DB 20; Length 531;
 Best Local Similarity 100.0%; Pred. No. 2.7e-254;
 Matches 531; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKPTSGPEEARROPDSIRVFASNCMHGIVHFGPGSLSLRGWMAAAVYLSVATFLYQV 60
 DB 1 MKPTSGPEEARROPDSIRVFASNCMHGIVHFGPGSLSLRGWMAAAVYLSVATFLYQV 60
 QY 61 AERRYRYREHHQALDERESHRLVFPAYVLCINPLRSLRSLTPNDLHMAGSALLGLDPA 120
 DB 61 AERRYRYREHHQALDERESHRLVFPAYVLCINPLRSLRSLTPNDLHMAGSALLGLDPA 120
 QY 121 EHAFLRALGRPPAPPGFMSPPTFDMAQLYARAGHSLLDMLDCRFRCGPGPENTTIF 180
 DB 121 EHAFLRALGRPPAPPGFMSPPTFDMAQLYARAGHSLLDMLDCRFRCGPGPENTTIF 180
 QY 181 TRMGKCYTFNSGADGAEELLTTTRGCMGNGLDIMLDVQEEYLPVWRDNEETPFEVGIRVQ 240
 DB 181 TRMGKCYTFNSGADGAEELLTTTRGCMGNGLDIMLDVQEEYLPVWRDNEETPFEVGIRVQ 240
 QY 241 IHSGEPPRIIDQGLGVSFGYQTFVSCQOQOQLSFLPPMGDCSSASLNPNYEPSPDPLG 300
 DB 241 IHSGEPPRIIDQGLGVSFGYQTFVSCQOQOQLSFLPPMGDCSSASLNPNYEPSPDPLG 300
 QY 301 SPSPSPSPYTLMGCRCLACTETRYVARKCGGRMYMPGDVPCSPQYKNCANPAIDAILR 360
 DB 301 SPSPSPSPYTLMGCRCLACTETRYVARKCGGRMYMPGDVPCSPQYKNCANPAIDAILR 360
 QY 361 KDCACACNPCASTRYAKELSMVRIPSRRAARFLARKLNRESEAYIAENVLALDIFEFLANTY 420
 DB 361 KDCACACNPCASTRYAKELSMVRIPSRRAARFLARKLNRESEAYIAENVLALDIFEFLANTY 420
 QY 421 EYVEOKKAYMSELGDIGOMGLFIGASLTLLTLEIDYCEVFRDVKVLYGFNNRHSOR 480
 DB 421 EYVEOKKAYMSELGDIGOMGLFIGASLTLLTLEIDYCEVFRDVKVLYGFNNRHSOR 480
 QY 481 HSTNTLQEGLSGSHRTQVPHLSGPRPPPCAVTKTSLASHRTCYLVTLQ 531
 DB 481 HSTNTLQEGLSGSHRTQVPHLSGPRPPPCAVTKTSLASHRTCYLVTLQ 531

RESULT 2
 AAY69181
 ID AAY69181 standard; Protein: 531 AA.

AC AAY69181;

DT 30-MAY-2000 (first entry)

DE A human acid-sensitive cationic channel 3 (hASIC3).

KM Neuronal acid-sensitive cation channel; ASIC; ASIC 3;
 KM proton-gated cation channel; biphasic desensitisation; amiloride;
 KM cation transport channel; acid sensor; pH detection.

OS Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

PF 05-AUG-1999; 99WO-1B01445.

PR 05-AUG-1999; 98US-0093508.

XX 05-AUG-1999; 98US-0093508.

Y bad date

*Good
 60/100 not good date*

PA (CNRS) CNRS CENT NAT RECH SCI.

XX *Madmann R, Bassiliana F, Lazdunski M, De Welle JR;*

XX WPI: 2000-195574/17.

DR N-PSDB: AA261203.

PT Novel human cation transport protein, Acid Sensing Ionic Channel 3 used
 PT to identify substances capable of modulating cation transport channel
 PT activity

PS Claim 4; Page 84; 84pp; English.

CC The present sequence represents a human neuronal acid-sensitive cation
 CC channel 3 (ASIC3) protein. The protein is a proton-gated cation
 CC channel subunit that has biphasic desensitisation kinetics with both
 CC a rapidly inactivating sodium-selective and a sustained component. The
 CC channels are sensitive to amiloride. The specification describes ASIC3
 CC proteins, which are expressed in the sensory neurons but not in the
 CC brain. The cation transport channel proteins can be used in methods to
 CC identify substances capable of modulating the activity of cation
 CC transport channels. The human ASIC3 protein is also an acid sensor,
 CC and might play an important role in the detection of lasting pH changes
 CC in humans.

XX Sequence 531 AA;

Query Match 99.4%; Score 2833; DB 21; Length 531;
 Best Local Similarity 99.2%; Pred. No. 1.2e-252;
 Matches 527; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKPTSGPEEARROPDSIRVFASNCMHGIVHFGPGSLSLRGWMAAAVYLSVATFLYQV 60
 DB 1 MKPTSGPEEARROPDSIRVFASNCMHGIVHFGPGSLSLRGWMAAAVYLSVATFLYQV 60
 QY 61 AERRYRYREHHQALDERESHRLVFPAYVLCINPLRSLRSLTPNDLHMAGSALLGLDPA 120
 DB 61 AERRYRYREHHQALDERESHRLVFPAYVLCINPLRSLRSLTPNDLHMAGSALLGLDPA 120
 QY 121 EHAFLRALGRPPAPPGFMSPPTFDMAQLYARAGHSLLDMLDCRFRCGPGPENTTIF 180
 DB 121 EHAFLRALGRPPAPPGFMSPPTFDMAQLYARAGHSLLDMLDCRFRCGPGPENTTIF 180
 QY 181 TRMGKCYTFNSGADGAEELLTTTRGCMGNGLDIMLDVQEEYLPVWRDNEETPFEVGIRVQ 240
 DB 181 TRMGKCYTFNSGADGAEELLTTTRGCMGNGLDIMLDVQEEYLPVWRDNEETPFEVGIRVQ 240
 QY 241 IHSGEPPRIIDQGLGVSFGYQTFVSCQOQOQLSFLPPMGDCSSASLNPNYEPSPDPLG 300
 DB 241 IHSGEPPRIIDQGLGVSFGYQTFVSCQOQOQLSFLPPMGDCSSASLNPNYEPSPDPLG 300
 QY 301 SPSPSPSPYTLMGCRCLACTETRYVARKCGGRMYMPGDVPCSPQYKNCANPAIDAILR 360
 DB 301 SPSPSPSPYTLMGCRCLACTETRYVARKCGGRMYMPGDVPCSPQYKNCANPAIDAILR 360
 QY 361 KDCACACNPCASTRYAKELSMVRIPSRRAARFLARKLNRESEAYIAENVLALDIFEFLANTY 420
 DB 361 KDCACACNPCASTRYAKELSMVRIPSRRAARFLARKLNRESEAYIAENVLALDIFEFLANTY 420
 QY 421 EYVEOKKAYMSELGDIGOMGLFIGASLTLLTLEIDYCEVFRDVKVLYGFNNRHSOR 480
 DB 421 EYVEOKKAYMSELGDIGOMGLFIGASLTLLTLEIDYCEVFRDVKVLYGFNNRHSOR 480
 QY 481 HSTNTLQEGLSGSHRTQVPHLSGPRPPPCAVTKTSLASHRTCYLVTLQ 531
 DB 481 HSTNTLQEGLSGSHRTQVPHLSGPRPPPCAVTKTSLASHRTCYLVTLQ 531

RESULT 3
 AAM88252
 ID AAM88252 standard; Protein: 549 AA.

AC AAM88252;

Query	Subject	Score	Length	Gap
1	1	94.9%	2706	549
2	2	93.9%	2706	549
3	3	93.9%	2706	549
4	4	93.9%	2706	549
5	5	93.9%	2706	549
6	6	93.9%	2706	549
7	7	93.9%	2706	549
8	8	93.9%	2706	549
9	9	93.9%	2706	549
10	10	93.9%	2706	549
11	11	93.9%	2706	549
12	12	93.9%	2706	549
13	13	93.9%	2706	549
14	14	93.9%	2706	549
15	15	93.9%	2706	549
16	16	93.9%	2706	549
17	17	93.9%	2706	549
18	18	93.9%	2706	549
19	19	93.9%	2706	549
20	20	93.9%	2706	549
21	21	93.9%	2706	549
22	22	93.9%	2706	549
23	23	93.9%	2706	549
24	24	93.9%	2706	549
25	25	93.9%	2706	549
26	26	93.9%	2706	549
27	27	93.9%	2706	549
28	28	93.9%	2706	549
29	29	93.9%	2706	549
30	30	93.9%	2706	549
31	31	93.9%	2706	549
32	32	93.9%	2706	549
33	33	93.9%	2706	549
34	34	93.9%	2706	549
35	35	93.9%	2706	549
36	36	93.9%	2706	549
37	37	93.9%	2706	549
38	38	93.9%	2706	549
39	39	93.9%	2706	549
40	40	93.9%	2706	549
41	41	93.9%	2706	549
42	42	93.9%	2706	549
43	43	93.9%	2706	549
44	44	93.9%	2706	549
45	45	93.9%	2706	549
46	46	93.9%	2706	549
47	47	93.9%	2706	549
48	48	93.9%	2706	549
49	49	93.9%	2706	549
50	50	93.9%	2706	549
51	51	93.9%	2706	549
52	52	93.9%	2706	549
53	53	93.9%	2706	549
54	54	93.9%	2706	549
55	55	93.9%	2706	549
56	56	93.9%	2706	549
57	57	93.9%	2706	549
58	58	93.9%	2706	549
59	59	93.9%	2706	549
60	60	93.9%	2706	549
61	61	93.9%	2706	549
62	62	93.9%	2706	549
63	63	93.9%	2706	549
64	64	93.9%	2706	549
65	65	93.9%	2706	549
66	66	93.9%	2706	549
67	67	93.9%	2706	549
68	68	93.9%	2706	549
69	69	93.9%	2706	549
70	70	93.9%	2706	549
71	71	93.9%	2706	549
72	72	93.9%	2706	549
73	73	93.9%	2706	549
74	74	93.9%	2706	549
75	75	93.9%	2706	549
76	76	93.9%	2706	549
77	77	93.9%	2706	549
78	78	93.9%	2706	549

Ybbs dds

Possible interaction w/ US Apple di

on gene clari

CC gustative perception, to cause analgesia or anaesthesia, or to
CC diagnose or treat any disorder related to abnormal expression of
CC hSLNAC1.
XX

SO Sequence 543 AA;

Query Match 91.1%; Score 2598; DB 20; Length 543;
Best Local Similarity 93.9%; Pred. No. 6,2e-231;
Matches 491; Conservative 4; Mismatches 12; Indels 16; Gaps 3;

QY 1 MKPSPGPEARPPSDIVAFNSCMHGLGVFGSGSLSRGMMAAVVLSVATFLVQ 60
DB 1 MKPSPGPEARPPSDIVAFNSCMHGLGVFGSGSLSRGMMAAVVLSVATFLVQ 60
QY 61 AERVYREFHQTALDERESHRLVFPVATLCINIPLRSLRTPNDLHMAGSALLGLDPA 120
DB 61 AERVYREFHQTALDERESHRLVFPVATLCINIPLRSLRTPNDLHMAGSALLGLDPA 120
QY 121 EHAFLRALGRPPAPPGFMPSPFTFDMQOLYARAGSLDMLDCRFRCQPCGFENFTTF 180
DB 121 EHAFLRALGRPPAPPGFMPSPFTFDMQOLYARAGSLDMLDCRFRCQPCGFENFTTF 180
QY 181 TRMGKCYTFNSGADGAEELTTTRGSMGNGLDIMLDVQOEYLPVWRDNEETPFEVGIRVQ 240
DB 181 TRMGKCYTFNSGADGAEELTTTRGSMGNGLDIMLDVQOEYLPVWRDNEETPFEVGIRVQ 240
QY 241 IHSQEEPIIDQLGLGVSPGYQTEFVSCQOQLSFLPPMGDCSSASLNPTEPEPSDPLG 300
DB 241 IHSQEEPIIDQLGLGVSPGYQTEFVSCQOQLSFLPPMGDCSSASLNPTEPEPSDPLG 300
QY 301 SPSPSPSPPYTLMGCRCLACETRYVARCKGCRMYMPGDVPCSPQOYKNCAPALDAILR 360
DB 301 SPSPSPSPPYTLMGCRCLACETRYVARCKGCRMYMPGDVPCSPQOYKNCAPALDAILR 360
QY 361 KDSCCPKPCASTRAKELSWRIPSRRAARFLARKLNRESEAYIAENVALDIFEALNY 420
DB 361 KDSCCPKPCASTRAKELSWRIPSRRAARFLARKLNRESEAYIAENVALDIFEALNY 420
QY 421 ETVQKKAEMSESLDLDIGOMGLFYGASLTLTLEILDYLCVEFRDKVLGYFWNRQHSOR 480
DB 421 ETVQKKAEMSESLDLDIGOMGLFYGASLTLTLEILDYLCVEFRDKVLGYFWNRQHSOR 480
QY 481 HSSNTLLOE-GLGSHRTQV---PHL-----SLGPRP 507
DB 481 HSSNTLLOE-GLGSHRTQV---PHL-----SLGPRP 507

RESULT 5
AAW88251 ID AAW88251 standard; Protein: 518 AA.

XX AC AAW88251;
XX DT 29-MAR-1999 (first entry)
XX DE Sodium channel receptor hSLNAC1 homologous polypeptide.
XX KM hSLNAC1; sodium channel receptor; human.
XX OS Homo sapiens.

AAW88251
BN NO9854366-A1.
PB 03-DEC-1998

PF 15-MAY-1998; 98MO-EP02884.

PR 30-MAY-1997; 97PF-0401196.

XX PA (SYNO) SYNTHETIC
XX PI Besnard F, Graham D, Renard S;
XX

*possible interaction
with protein 420*

DR WPI: 1999-070215/06.
DR N-PSDB: AAW84190.

XX A new sodium channel receptor - useful for, e.g. treatment of
XX neuronal degenerate problems, Alzheimer's, Parkinson's disease and
XX morphine dependence
XX

PS Claim 24; Page 41-42; 63pp; English.

CC This polypeptide shows homology to the novel human sodium channel
CC receptor hSLNAC1 (see AAW88251). It is encoded by a cDNA clone (see
CC AAW84190) derived from the human cerebellum. hSLNAC1 is a member of
CC a new class of sodium channel proteins that may be responsible for
CC some nervous system transmissions, or may be used as a target to
CC regulate some transmissions linked to various pathologies.
CC Agonists and antagonists of hSLNAC1 activity can be used to treat
CC e.g. neurodegenerative problems, morphine or nicotine dependency,
CC or cancer.
XX

SO Sequence 518 AA;

Query Match 87.0%; Score 2481; DB 20; Length 518;
Best Local Similarity 94.0%; Pred. No. 3.7e-220;
Matches 468; Conservative 4; Mismatches 10; Indels 16; Gaps 3;

QY 26 MHGLGVFGPSLSLRGMMAAVVLSVATFLVQAEVRYRREFHQTALDERESHRLV 85
DB 1 MHGLGVFGPSLSLRGMMAAVVLSVATFLVQAEVRYRREFHQTALDERESHRLV 85
QY 86 FPVATLCINIPLRSLRTPNDLHMAGSALLGLDPAEHAFLRALGRPPAPPGFMPSPFD 145
DB 61 FPVATLCINIPLRSLRTPNDLHMAGSALLGLDPAEHAFLRALGRPPAPPGFMPSPFD 120
QY 146 MAOLYARAGHSLDMLDCRFRCQPCGFENFTTFTRMGKCYTFNSGADGAEELTTTRG 205
DB 121 MAOLYARAGHSLDMLDCRFRCQPCGFENFTTFTRMGKCYTFNSGADGAEELTTTRG 180
QY 206 MNGNGLDMLDVQOEYLPVWRDNEETPFEVGIRVQIHSQEEPIIDQLGLGVSPGYQTEFV 265
DB 181 MNGNGLDMLDVQOEYLPVWRDNEETPFEVGIRVQIHSQEEPIIDQLGLGVSPGYQTEFV 240
QY 266 SCQOQOQLSFLPPMGDCSSASLNPTEPEPSDPLGSPSPPYTLMGCRCLACETRYVA 325
DB 241 SCQOQOQLSFLPPMGDCSSASLNPTEPEPSDPLGSPSPPYTLMGCRCLACETRYVA 300
QY 326 RKCCGRMYMPGDVPCSPQOYKNCAPALDAILRKDSCACPNPCASTRYAKELSMWRIP 385
DB 301 RKCCGRMYMPGDVPCSPQOYKNCAPALDAILRKDSCACPNPCASTRYAKELSMWRIP 360
QY 386 SRAARFLARKLNRESEAYIAENVALDIFEALNYETVQKKAEMSESLDLDIGOMGLF 445
DB 361 SRAARFLARKLNRESEAYIAENVALDIFEALNYETVQKKAEMSESLDLDIGOMGLF 420
QY 446 IGASLTLTLEILDYLCVEFRDKVLGYFWNRQHSSTNLOE-GLGSHRTQV---PHL 501
DB 421 IGASLTLTLEILDYLCVEFRDKVLGYFWNRQHSSTNLOE-GLGSHRTQV---PHL 480
QY 502 -----SLGPRP 507
DB 481 LPCHTALDLVSSSEPRP 498

RESULT 6
AAW68508 ID AAW68508 standard; Protein: 533 AA.

XX AC AAW68508;

XX DT 02-FEB-1999 (first entry)

XX DE Rat acid sensing ionic channel DRASIC.

XX KM Rat; neuronal cationic channel; amiloride; proton; ASIC; brain; probe;

KM acid sensing ionic channel: hybridisation: primer: PCR: amplification:
 KM modulator: acidity: nociception: pain: taste: inflammation: ischaemia;
 KM tumour: cerebral neurodegeneration: transgenic animal: knockout animal;
 KM gene therapy: Alzheimer's; Parkinson's; Huntington's; disease;
 KM amyotrophic lateral sclerosis; cerebellar ataxia.

OS Rattus sp.

PN MO9835034-A1.

XX 13-AUG-1998.

PD 11-FEB-1998;

XX 9800-0000270.

XX 28-JUL-1997; 97FR-0009587.

XX 11-FEB-1997; 97FR-0001574.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX Basillana F, Champigny G, Heurteaux C, Lazdunski M;

XX Waldegg R, Lingueglia E;

XX WPI: 1998-447231/38.

XX N-PSDB: AAV60843.

XX Protein comprising proton-sensitive neuronal channel - useful for

XX screening for analgesics and for treating neurodegeneration

XX Claim 6; Page 38-40; 64pp; French.

CC This sequence represents the rat Acid Sensing Ionic Channel (ASIC)
 CC DRASIC protein, a member of the neuronal cationic channel family that
 CC are sensitive to amiloride and activated by protons. The DRASIC gene
 CC is expressed in sensory neuronal cell rather than in the brain as with
 CC other members of the ASIC gene family. The protein can be used to
 CC screen for modulators of these channels, particularly to identify
 CC compounds that modulate perception of acidity, as regards nociception
 CC (pain) rather than taste. These compounds are used to treat or prevent
 CC pain associated with acidity (e.g. in cases of inflammation, ischaemia
 CC or some tumours) and as inhibitors of neurodegeneration caused by
 CC overexpression of the channels. Antibodies to the protein are used to
 CC detect the channels in tissues, and to act therapeutically as channel
 CC modulators. The nucleic acid can be used to generate transgenic,
 CC particularly knockout, animals for studying ASIC-related disorders,
 CC also for gene therapy. The channel protein, or its (ant)agonists, can
 CC be used to treat or prevent cerebral neurodegenerative conditions (e.g.
 CC Alzheimer's, Parkinson's or Huntington's diseases, amyotrophic lateral
 CC sclerosis or cerebellar ataxia).

SQ Sequence 533 AA;

Query Match 85.8%; Score 2447; DB 19; Length 533;

Best Local Similarity 83.5%; Pred. No. 5.3e-217;

Matches 445; Conservative 49; Mismatches 37; Indels 2; Gaps 2;

DB 1 MKPTSGPEEA-RPSPDIFVASCNMGHGFVFGPSLILRGMAAAVLSVAFVLYQ 59

DB 1 MKPRSLERAPORROASDIRVASSCTMHGHTFGGGLTLRGMAVAVLSLAFVLYQ 60

DB 60 VAEVRYREBFHQTALDERESHRLVPAVTLICNINPLRSRLTPNDLHWAGSALLGLDP 119

DB 61 VAEVRYREBFHQTALDERESHRLVPAVTLICNINPLRSRLTPNDLHWAGSALLGLDP 120

DB 120 AEAALALRALGRPPAPGPPSTFPMALQYARAGSLDMLDCFRGQPCPENFTTI 179

DB 121 AEAALALRALGRPPAPGPPSTFPMALQYARAGSLDMLDCFRGQPCPENFTTI 180

DB 180 FTRMGKCYFNSGADGAEILLTTRGSGMGLDMLDVOOEYLPVWRDNEPFEFGIRV 239

DB 181 FTRMGKCYFNSGADGAEILLTTRGSGMGLDMLDVOOEYLPVWRDNEPFEFGIRV 240

DB 240 QIHSGEPPILDLGLGVSPGYQTFVSCQOQOLSLPPWGDSSSLNP-NYPEPSPD 298

DB 241 QIHSGEPPILDLGLGVSPGYQTFVSCQOQOLSLPPWGDSSSLNP-NYPEPSPD 300

QY 299 LGSPPSPSPPTLTMGCRACETRYARKCGCMYMPEDVPYCSQYQKNCAPLADI 358

DB 301 LGSPPSPSPPTLTMGCRACETRYARKCGCMYMPEDVPYCSQYQKNCAPLADI 360

QY 359 LRRDSCAPNCPASTRYAKELSMVRIPSRRAARFLARKINRSRPAVLAENVLADIFEAL 418

DB 361 LRRDSCAPNCPASTRYAKELSMVRIPSRRAARFLARKINRSRPAVLAENVLADIFEAL 420

QY 419 NYETVEOKKAYEMSELLDYGOMGLFISASLTITLLEIDYCEVFRDVLGFYNNRHS 478

DB 421 NYETVEOKKAYEMSELLDYGOMGLFISASLTITLLEIDYCEVFRDVLGFYNNRHS 480

QY 479 QHRSSTNLQEGISHRTQVPHLSLGRPPPTPCAVTKTSLASHRTCYLVTL 531

DB 481 QHRSSTNLQEGISHRTQVPHLSLGRPPPTPCAVTKTSLASHRTCYLVTL 533

RESULT 7

AA69179

AC AAV69179;

DT 30-MAY-2000 (first entry)

DE A rat acid-sensitive cationic channel 3 (rASIC3).

KM Neuronal acid-sensitive cation channel; ASIC; ASIC 3;

KM proton-gated cation channel; biphasic desensitisation; amiloride;

XX cation transport channel; acid sensor; pH detection.

XX Rattus sp.

XX WO200008149-A2

XX 17-FEB-2000

XX 05-AUG-1999; 199WO-1B01445.

XX 05-AUG-1998; 98US-0095408.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX Waldmann R, Basillana F, Lazdunski M, De Weille JR;

XX WPI: 2000-195574/17.

XX N-PSDB: AAV61201.

XX Novel human cation transport protein, Acid Sensing Ionic Channel 3 used

XX to identify substances capable of modulating cation transport channel

XX activity

XX Disclosure; Page 77-79; 84pp; English.

XX The present sequence represents a rat neuronal acid-sensitive cation

XX channel 3 (ASIC3) protein. The protein is a proton-gated cation

XX channel subunit that has biphasic desensitisation kinetics with both

XX a rapidly inactivating sodium-selective and a sustained component. The

XX channels are sensitive to amiloride. The specification describes ASIC3

XX proteins, which are expressed in the sensory neurons but not in the

XX brain. The cation transport channel proteins can be used in methods to

XX identify substances capable of modulating the activity of cation

XX transport channels. The human ASIC3 protein is also an acid sensor,

XX and might play an important role in the detection of lasting pH changes

XX in humans.

XX Sequence 533 AA;

Query Match 85.8%; Score 2447; DB 21; Length 533;

Best Local Similarity 83.5%; Pred. No. 5.3e-217;

Matches 445; Conservative 49; Mismatches 37; Indels 2; Gaps 2;

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QY 1 MKPTSGPEEA-RROPSDIRVFASNCMHGLGHVFGPSLSLIRGMAAVALSVATFLYO 59
DB 1 MKPRSGLEBAQRASDIRVFASCTMGLGHIIFGPGGLTLARGLMAVATVLLSLAFLQ 60
QY 60 VAERRYRREFHQAALDERESHRLVFPVAVTLCNTNPLRSLRFLTPNDLMAGSALLGDP 119
DB 61 VAERRYRREFHQAALDERESHRLVFPVAVTLCNTNPLRSLRFLTPNDLMAGSALLGDP 120
QY 120 AEHAFLNALGRPPAPPGPMSPPTFDMQOLYARAGSHSLDDMLDRCRFGOPCGPENTFI 179
DB 121 AEHAFLNALGRPPAPPGPMSPPTFDMQOLYARAGSHSLDDMLDRCRFGOPCGPENTFI 180
QY 180 FTRMGKCYTFNSGADGAEILLTTRGSGMGNGLDIMLDVQOEYLPVWRDNEETPFEVGIRV 239
DB 181 FTRMGKCYTFNSGADGAEILLTTRGSGMGNGLEIMLDVQOEYLPVWRDNEETPFEVGIRV 240
QY 240 QIHSGEPPPIIDQLGGLVSPGYQTVSCQOQOOLFLPPWGCSSASLNP-NYEPSPDP 298
DB 241 QIHSGDEPPPIIDQLGGLVSPGYQTVSCQOQOOLFLPPWGCSSASLNPDPDFDEPSPDP 300
QY 299 LGSPSPSPPTTLMGCRACETRVRVARKCGCRMYVMPGDVPCSPQOYKNCAPALDAI 358
DB 301 LGSPSPSPPTTLMGCRACETRVRVARKCGCRMYVMPGDVPCSPQOYKNCAPALDAI 360
QY 359 LRKQSCAPNPDCASTRYAKELSMVRIPSRAAARFLARKLRSEAYIAENVLALDIFFEAL 418
DB 361 LRKQSCAPNPDCASTRYAKELSMVRIPSRAAARFLARKLRSEAYIAENVLALDIFFEAL 420
QY 419 NYETVEOKKAYEMSELDDIGOMGLFTGASLLTLEILDYCEVFRDQVGLGYFNNRQHS 478
DB 421 NYEAEVOKKAYEMSELDDIGOMGLFTGASLLTLEILDYCEVFRDQVGLGYFNNRQHS 480
QY 479 ORHSSTNLQEGLSHRTQVPHLSGRPPPTPCAVTKTSLASHRTCYLVNQL 531
DB 481 ORHSSTNLQEGLSHRTQVPHLSGRPPPTPCAVTKTSLASHRTCYLVNQL 533

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RESULT 8
AAM68506
AAM68506 standard; Protein: 512 AA.

AC AAM68506;
DT 02-FEB-1999 (first entry)

DE Human acid sensing ionic channel MDEC.
KW Human; neuronal cationic channel; amiloride; proton; ASIC; brain; probe;
KW acid sensing ionic channel; hybridisation; primer; PCR; amplification;
KW modulator; acidity; nociception; pain; taste; inflammation; ischaemia;
KW tumour; cerebral neurodegeneration; transgenic animal; knockout animal;
KW gene therapy; Alzheimer's; Parkinson's; Huntington's; disease;
KW amyotrophic lateral sclerosis; cerebellar ataxia.

OS Homo sapiens.
XX
XX MO9835034-A1.
XX
XX PD 13-AUG-1998.
XX
XX PE 11-FEB-1998; 98MO-FR00270.
XX
XX PR 28-JUL-1997; 97FR-0009587.
XX
XX PR 11-FEB-1997; 97FR-0001574.
XX
XX PA (CNRS) CNRS CENT NAT RECH SCT.
XX
XX PI Bassilana F, Champigny G, Heurteaux C, Lazdunski M;
XX Waldmann R, Lingueglia E;
XX WPI: 1998-447231/38.
XX DR N-PSDB; AAV60841.
DR

```

XX protein comprising proton-sensitive neuronal channel - useful for
PT screening for analgesics and for treating neurodegeneration
PS
XX Claim 4; Page 31-33; 64pp; French.
XX
CC This sequence represents the human Acid Sensing Ionic Channel (ASIC)
CC protein MDEC, a member of the neuronal cationic channel family that are
CC sensitive to amiloride and activated by protons. The protein can be
CC used to screen for modulators of these channels, particularly to identify
CC compounds that modulate perception of acidity, as regards nociception
CC (pain) rather than taste. These compounds are used to treat or prevent
CC or some tumours) and as inhibitors of neurodegeneration caused by
CC overexpression of the channels. Antibodies to the protein are used to
CC detect the channels in tissues, and to act therapeutically as channel
CC modulators. The nucleic acid can be used to generate transgenic,
CC particularly knockout, animals for studying ASIC-related disorders,
CC also for gene therapy. The channel protein, or its (ant)agonists, can
CC be used to treat or prevent cerebral neurodegenerative conditions (e.g.
CC Alzheimer's, Parkinson's or Huntington's diseases, amyotrophic lateral
CC sclerosis or cerebellar ataxia.
CC
SQ Sequence 512 AA;

```

Query Match 47.9%; Score 1365; DB 19; Length 512;
Best Local Similarity 50.6%; Pred. No. 3,8e-117;
Matches 255; Conservative 83; Mismatches 140; Indels 26; Gaps 5;

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QY 7 PEARROPSDIRVFASNCMHGLGHVFGPSLSLIRGMAAVALSVATFLYOYQAEVRY 66
DB 7 PSEGLSPSSIIQIFANTSLHGRHIFVYGLPIRRLVMAVAGSLGLLVESSERSVY 66
QY 67 YREFHQAALDERESHRLVFPVAVTLCNTNPLRSLRFLTPNDLMAGSALLGDP----PAE 121
DB 67 YFSYQHVTKVDEVAQSLVFPVAVTLCNLTNGFRFSRLTNDLYHAGELLALDVLNIQIDP 126
QY 122 HAA--FLRALGRPPAPPGPMSPPTFDMQOLYARAGSHSLDDMLDRCRFGOPCGPENTFI 178
DB 127 HADPSVLEALRQKANFNHYKQ-QFSMLERLHRYGHDLMKMLCKRGQEGCHQDFTT 185
QY 179 IFTRMGKCYTFNSGADGAEILLTTRGSGMGNGLDIMLDVQOEYLPVWRDNEETPFEVGIR 238
DB 186 VFTKYGKCYTFNSGADGAEILLTTRGSGMGNGLEIMLDVQOEYLPVWRDNEETPFEVGIR 245
QY 239 VOIHSQSEPPPIIDQLGGLVSPGYQTVSCQOQOOLFLPPWGCSSASLNPNYEPSPDP 298
DB 246 VOIHSQSEPPPIIDQLGGLVSPGYQTVSCQOQOOLFLPPWGCSSASLNPNYEPSPDP 298
QY 299 LGSPSPSPPTTLMGCRACETRVRVARKCGCRMYVMPGDVPCSPQOYKNCAPALDAI 358
DB 299 LGSPSPSPPTTLMGCRACETRVRVARKCGCRMYVMPGDVPCSPQOYKNCAPALDAI 358
QY 359 LRKQSCAPNPDCASTRYAKELSMVRIPSRAAARFLARKLRSEAYIAENVLALDIFFE 416
DB 351 AEKDSNYCLCRPTCNLTTRYNELSMVKIPSTSAVLEKFKKSEKSEYISENIVLIDFEE 410
QY 417 ALNVEVOKKAYEMSELDDIGOMGLFTGASLLTLEILDYCEVFRDQVGLGYFNNRQ 476
DB 411 ALNVEVOKKAYEMSELDDIGOMGLFTGASLLTLEILDYCEVFRDQVGLGYFNNRQ 476
QY 477 HSORHSSTNLQEGLSHRTQVPH 500
DB 471 DEGSIDENVSTCDMPNHSFTISH 494

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RESULT 9
AAM93420
AAM93420 standard; Protein: 512 AA.

AC AAM93420;
DT 14-JUN-1999 (first entry)


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xx Sequence 512 AA: 47.9% Score 1365; DB 21; Length 512;
SQ Query Match Best Local Similarity 50.6%; Pred. No. 3.8e-117;
Matches 255; Conservative 83; Mismatches 140; Indels 26; Gaps 5;

OY 7 PEARRPSDIRVAFASNCMHGIFGPGSLSLRGMMAAVALSVATFLYQVAREVRY 66
DB 7 PEGSLDPSISIOIFANTSTLHGIRHIFVYGPILIRVLAVAFVSGLLGVSSRSRY 66
OY 67 YEFHQTALDRSHRLVFPVATVLCNINPLRSRLTPVDLHWAGSALLGLD-----PAE 121
DB 67 YESYOHVKKVDEVVAOSLTFPAVTTCNLNGFRFSRLTTNDLVHAGELLALLDVNLQIDPP 126
OY 122 HAA-----FLRALGRPPAPPCGFMDMAQLVARAGHSIDMLDLCRFRGOCGPENFTT 178
DB 127 HLAADSVLEALQKANKFKRYKPK-QFSMLEFLHRVGHDLKMDMLCKFKGQCGHODFTT 185
OY 179 IFTRMGKCYTFNSGADGAELLTTTRGCMGGLDMLDVQOEYLPVWRDNEETPEVGI 238
DB 186 VFTKYGKCYMFNSGEGDKPLTTTKVGGTNGLEIMLDIQDEYLPIMGTEETFEAGVK 245
OY 239 VOIHQDEEPTIDGLGVSFGYOTFVSCQQOQLSFLPPMGDCSSASLNPNYEPSPDP 298
DB 246 VOIHQSEEPFIOELGFGVAPGFQTFVATQEQRLTYLLPPPMGECSSSEGLDF----- 298
OY 299 LGSPPSPSPPYTLTMGCRCLACETRYVARCKGCRMYVMPGDVPCSPQOYKNCAPDAI 358
DB 299 -----FPVYSTACRIDCETRYIVENCRCRWYHMPGDAPFCPTPEQKCEAPALGL 350
OY 359 LRKDS--CACPNPCASTRYAKELSVRIIPSRAAARFLARKLNSEAYIAENVLALDIFE 416
DB 351 AEKDNYNCCICRTPCMLTRYKNKELSMVKIPSKTSAKYLEKFKNSEKYEISENITLVDIFE 410
OY 417 ALNVTYQKAKYEMSELLDQIGOMGLFIGASLTLTLEIDYLCGEVFRDYLKGFWMNQ 476
DB 411 ALNVTYEQKAKYEVALLGDIGOMGLFIGASLTLTLEIDYLYELKLEKLLDLGKEE 470
OY 477 HSQRHSTNLQELGSHRTQVPH 500
DB 471 DEGSHDENVSTCDTMRPNHSETISH 494

RESULT 11
AA03186 ID AAY03186 standard; Protein: 513 AA.
XX AC AAY03186;
XX DT 16-JUN-1999 (first entry)
XX DE Rat Acid sensitive ion channel protein sequence.
XX KW Acid sensitive ion channel; rat; ASIC; pH mediated pain disorder;
XX KM Ischaemia; gene therapy; proton-gated ion channel.
XX OS Rattus sp.
XX PN MO9911784-A1.
XX PD 11-MAR-1999.
XX PF 28-AUG-1998; 98WO-GB02609.
XX PR 29-AUG-1997; 97GB-0018365.
XX PA (UNLO ) UNIV COLLEGE LONDON.
XX PI Akopian AN, Chen C, England S, Wood JN;
XX DR WPI: 1999-205188/17.
DR N-PSDB: AAX28161.

```

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xx Acid sensitive ion channel (ASIC) proteins - useful in gene therapy
xx for treatment of pH mediated pain disorders
xx Claim 5; Page 43-47; 62pp; English.
xx This sequence represents an acid sensitive ion channel (ASIC) of the
xx invention, isolated from rat dorsal root ganglion. Antisense ASIC DNA or
xx RNA is useful in gene therapy for downgrading expression of ASIC protein,
xx for pH mediated pain disorders e.g. in ischemia. The vectors are useful
xx for incorporating ASIC DNA or RNA for use in gene therapy. Proton-gated
xx ion channel agonists and antagonists are identified using cells
xx transformed with ASIC DNA by allowing interaction between the candidate
xx substance and ASIC protein in the membrane, and measuring interaction
xx and/or cell response. Partial agonists and antagonists can be identified
xx by their ability to block the response of the cell to present in a
xx solution of a given acid pH or any agonist. The hybridisation probes are
xx useful for screening libraries for ASIC DNA or RNA.

SQ Sequence 513 AA: 47.0% Score 1340; DB 20; Length 513;
Query Match Best Local Similarity 49.8%; Pred. No. 7.7e-115;
Matches 256; Conservative 83; Mismatches 141; Indels 34; Gaps 7;

OY 1 MKPTSGPEARRPSDIRVAFASNCMHGIFGPGSLSLRGMMAAVALSVATFLYQV 60
DB 1 MEAGSELDEGDSPDLVAFANSTLHGASHVEFGGPGPQALMAVAFVIALGAFLCQV 60
OY 61 AERVYRYEFHQTALDRSHRLVFPVATVLCNINPLRSRLTPVDLHWAGSALLGLDPA 120
DB 61 GDRVAYRYEFTPLTDLDEVAISELVEFPVATFCTNAVRLSOLSTYDLYL-APMLGLDES 119
OY 121 EHAATFLRALGRPPAPPCGFMDMAQLVARAGHSIDMLDLCRFRGOCGPENFTTIF 180
DB 120 DDPGVPPLA---PPGPEARSGER-FNLHRFYRNSCHRLDMLLYCYCGPGCPHNFVYF 175
OY 181 TRMGKCYTFNSGADGAELLTTTRGCMGGLDMLDVQOEYLPVWRDNEETPEVGI 240
DB 176 TRYGKCYTFNSGODRPRKTKWGGTNGLEIMLDIQDEYLPVWGEMDETSFEAGIKVQ 235
OY 241 IHSQDEEPTIDGLGVSFGYOTFVSCQQOQLSFLPPMGDCSSASLNPNYEPSPDLG 300
DB 236 IHSQDEEPTIDGLGFGVAPGFQTFVSCQEQRLTYLPSWGTCAVATMDSPD----- 286
OY 301 SPSPSPSPPYTLTMGCRCLACETRYVARCKGCRMYVMPGDVPCSPQOYKNCAPDAI 360
DB 287 -----PDSYSTTACRIDCETRYIVENCRCRWYHMPGDAPCTPEQKCEADPALDIFE 340
OY 361 KDS--CACPNPCASTRYAKELSVRIIPSRAAARFLARKLNSEAYIAENVLALDIFE 418
DB 341 KDQECVCCEMPENLTRYKELSMVKIPSKASAKYLEKFKNSEQYIGENITLVDIFE 400
OY 419 NYETVEOKKAYEMSELLDQIGOMGLFIGASLTLTLEIDYLCGEVFRDYLKGFWMNQ 478
DB 401 NYETVEOKKAYEIALGLDQIGOMGLFIGASLTLTLEIDYLYELKLEKLLDLGKEE 476
OY 479 QRHSTNLQELGSHRTQVPHSLGPPRPPPPC 512
DB 457 QKAKRSSADKGA-----LSLDVYKRHNPC 482

RESULT 12
AA068507 ID AAM68507 standard; Protein: 559 AA.
XX AC AAM68507;
XX DT 02-FEB-1999 (first entry)
XX DE Rat acid sensing ionic channel 1B.
XX KM Rat; neuronal cationic channel; amiloride; proton; ASIC; brain; probe;

```

KW acid sensing ionic channel; hybridisation; primer; PCR; amplification;
 KW modulator; acidity; nociception; pain; taste; inflammation; ischaemia;
 KW tumour; cerebral neurodegeneration; pain; taste; inflammation; ischaemia;
 KW gene therapy; Alzheimer's; Parkinson's; Huntington's; disease;
 KW amyotrophic lateral sclerosis; cerebellar ataxia.
 XX Rattus sp.
 OS
 XX MO9835034-A1.
 XX
 PD 13-AUG-1998.
 XX
 XX 11-FEB-1998; 98WO-FR00270.
 XX
 XX 28-JUL-1997; 97FR-0009587.
 PR 11-FEB-1997; 97FR-0001574.
 XX
 XX (CNRS) CNRS CENT NAT RECH SCI.
 PA
 PI Bassilana F, Champigny G, Heurteaux C, Lazdunski M;
 PI Waldmann R, Lingueglia E;
 DR WPI: 1998-447231/38.
 DR N-PSDB; AAV60842.
 XX
 PT protein comprising proton-sensitive neuronal channel - useful for
 PT screening for analgesics and for treating neurodegeneration
 XX
 PS Claim 5; Page 34-37; 64pp; French.
 XX
 CC This sequence represents the rat Acid Sensing Ionic Channel (ASIC) 1B
 CC protein, a member of the neuronal cationic channel family that are
 CC sensitive to amiloride and activated by protons. The protein can be
 CC used to screen for modulators of these channels, particularly to identify
 CC compounds that modulate perception of acidity, as regards nociception
 CC (pain) rather than taste. These compounds are used to treat or prevent
 CC pain associated with acidity (e.g. in cases of inflammation, ischaemia
 CC or some tumours) and as inhibitors of neurodegeneration caused by
 CC overexpression of the channels. Antibodies to the protein are used to
 CC detect the channels in tissues, and to act therapeutically as channel
 CC modulators. The nucleic acid can be used to generate transgenic,
 CC particularly knockout, animals for studying ASIC-related disorders,
 CC also for gene therapy. The channel protein, or its (antagonists, can
 CC be used to treat or prevent cerebral neurodegenerative conditions (e.g.
 CC Alzheimer's, Parkinson's or Huntington's diseases, amyotrophic lateral
 CC sclerosis or cerebellar ataxia.
 CC
 SQ Sequence 559 AA;
 Query Match 46.9%; Score 1337; DB 19; Length 559;
 Best Local Similarity 49.8%; Pred. No. 1.6e-114;
 Matches 256; Conservative 82; Mismatches 142; Indels 34; Gaps 7;
 OY 1 MKPTSGPEARARQPSDIRFASNCMHGIGHVFGPGSLLRGGMMAAAVVLVATFLYGV 60
 DB 47 MARGSELDEBGDSPRDVLAFAFNSCTFHGASHVFEVGGPPKALNAVAIVLGAFLCY 106
 OY 61 AERYRYREFFHQALDERESHRLVFPVATLONINPLRRSRLLTPNDLHWAGSALLGLDPA 120
 DB 107 GBRVAVYLYSTPHTLDEVAATELVFPAVTCFNNAVRLSQSYDPLVL-APMLGLDES 165
 OY 121 EHAALRLAGRPARPAGFPSPFTFMAOLXARAGSLDMLDCFRQPCGPEPNTTIF 180
 DB 166 DDPGVPLA--PPGEATSGEP-FNLHFRYNSCHRLEDMLLYCSYCGGCPGPHNVSVF 221
 OY 181 TRMGKCYTFNSGADAEALITTRGGMGNGLDITMLDVQCEELPVARNDETPEFVGIRVQ 240
 DB 222 TRYGKCYTFNSGODGRPRKTKMGKGTGNGLEITMLDIQODEYLPVNGETDSTFEAGIKVQ 281
 OY 241 IHSQEPPIIDGLGVSDEYQTEVSCQOQSLPPLPPMGDCSSASLNDNYPEPSPDLG 300
 DB 282 IHSODEPPIIDGLGVAAGFQTFVSCQORLILYLPSPWGTCNAVTVMDSDF----- 332

OY 301 SPSPSPPYTLMGCLACETRYVARKCCRMVYMGDVPVCSPOQYKNCAPDAIDLR 360
 DB 333 -----FDSYSTTACRIDCETRIYVENCNCRWVHPGDAPYCTPEYKRCADPAIDFLVE 386
 OY 361 KDS--CACPNPCASTRYAKELSWRIPSRRAARFLARKINREAVYIAENVLADIFFEAL 418
 DB 387 KQEVYCVCEMPCNLTRYGKELSKVYKPSKASAKYLAKEFKNSQYIGENILVYDIFFEVL 446
 OY 419 NYETVQKKAYEMSELLGPIGOMGLFAGASLITLIEILDYLCVPRQKVLGYFMNRQHS 478
 DB 447 NYETIEQKKAYETAGLIGIGOMGLFAGASLITLIEILFDYAEVYIKHRLC---RKGK 502
 OY 479 ORHSTFNLQEGLSHRTQVPHLSLGRPPPTPC 512
 DB 503 QKEAKRSSADKVA-----LSLDVYKRHNPC 528
 RESULT 13
 AAY69178
 ID AAY69178 standard; Protein; 559 AA.
 XX
 XX AAY69178;
 AC
 XX
 XX 30-MAY-2000 (first entry)
 DT
 XX
 DE A rat acid-sensitive cationic channel 1B (rASIC1B).
 XX
 KW Neuronal acid-sensitive cation channel; ASIC; ASIC 1B;
 KW proton-gated cation channel; biphasic desensitisation; amiloride;
 KW cation transport channel; acid sensor; pH detection.
 XX
 OS Rattus sp.
 XX
 XX WO200008149-A2.
 XX
 PD 17-FEB-2000.
 XX
 PF 05-AUG-1999; 99WO-IB01445.
 XX
 PR 05-AUG-1998; 98US-0095408.
 XX
 PA (CNRS) CNRS CENT NAT RECH SCI.
 PI Waldmann R, Bassilana F, Lazdunski M, De Welle JR;
 PI WPI: 2000-195574/17.
 DR N-PSDB; AAZ61200.
 DR
 XX
 PT Novel human cation transport protein, Acid Sensing Ionic Channel 3 used
 PT to identify substances capable of modulating cation transport channel
 PT activity -
 PS
 PS Disclosure; Page 73-76; 84pp; English.
 XX
 CC The present sequence represents a rat neuronal acid-sensitive cation
 CC channel 1B (ASIC1B) protein. The protein is a proton-gated cation
 CC channel subunit that has biphasic desensitisation kinetics with both
 CC a rapidly inactivating sodium-selective and a sustained component. The
 CC channels are sensitive to amiloride. The specification describes ASIC3
 CC proteins, which are expressed in the sensory neurons but not in the
 CC brain. The cation transport channel proteins can be used in methods to
 CC identify substances capable of modulating the activity of cation
 CC transport channels. The human ASIC3 protein is also an acid sensor,
 CC and might play an important role in the detection of lasting pH changes
 CC in humans.
 CC
 SQ Sequence 559 AA;
 Query Match 46.9%; Score 1337; DB 21; Length 559;
 Best Local Similarity 49.8%; Pred. No. 1.6e-114;
 Matches 256; Conservative 82; Mismatches 142; Indels 34; Gaps 7;
 OY 1 MKPTSGPEARARQPSDIRFASNCMHGIGHVFGPGSLLRGGMMAAAVVLVATFLYGV 60

Protein compitling proton-sensitive neuronal channel - useful for

[illegible]

XX Rat Acid sensitive ion channel alpha protein sequence.
 DE Acid sensitive ion channel; rat; ASIC; pH mediated pain disorder;
 KW Ischaemia; gene therapy; proton-gated ion channel.
 XX Rattus sp.
 OS WO9911784-A1.
 PN 11-MAR-1999.
 PD 28-AUG-1998; 98WO-GB02609.
 XX 29-AUG-1997; 97GB-0018365.
 PR (UNLO) UNITV COLLEGE LONDON.
 XX Akopian AN, Chen C, England S, Wood JN,
 PI WPI, 1999-205188/17.
 DR
 XX Acid sensitive ion channel (ASIC) proteins - useful in gene therapy
 PT for treatment of pH mediated pain disorders
 PS
 XX Disclosure: Page 55-57; 62pp; English.
 CC This sequence represents an acid sensitive ion channel (ASIC) of the
 CC invention, isolated from rat dorsal root ganglion. Antisense ASIC DNA or
 CC RNA is useful in gene therapy for downgrading expression of ASIC protein,
 CC for pH mediated pain disorders e.g. in ischaemia. The vectors are useful
 CC for incorporating ASIC DNA or RNA for use in gene therapy. Proton-gated
 CC ion channel agonists and antagonists are identified using cells
 CC transformed with ASIC DNA by allowing interaction between the candidate
 CC substance and ASIC protein in the membrane, and measuring interaction
 CC and/or cell response. Partial agonists and antagonists can be identified
 CC by their ability to block the response of the cell to present in a
 CC solution of a given acid pH or any agonist. The hybridisation probes are
 CC useful for screening libraries for ASIC DNA or RNA.
 CC
 XX
 SQ Sequence 526 AA;

Query Match 46.6%; Score 1329; DB 20; Length 526;
 Best Local Similarity 49.5%; Pred. No. 8.2e-114;
 Matches 257; Conservative 79; Mismatches 127; Indels 56; Gaps 8;

QY 13 QPSDIFVPAVNSCMHGLVHFGPGLSLRGMMAAVALSVATFLYQVARYRYREFFH 72
 DB 14 QPVSIDAFASSSTHGLAHFYSERLSLRKALMALCFLSLAVLGCCTERVQYFCYHH 73
 QY 73 QVALDERESHRLVPAVTLCTNINPLRSRLTPDLMWAGS--ALLG----- 116
 DB 74 VTKLDVAASQLTFEPAVTLCTNLEFFRSQVSKNDLHAAGELLALLNNRYEIPDTQADEK 133
 QY 117 -LDPAEHAFLRALGRPPAPGFMPSPTFDMQVYARAGSHLDDMLDCFRGQCPGEN 175
 DB 134 QLEIIGDKANFRS-----FKPKP-FNMRFFYDRAGHDIRDMILSCHFRGEACSAED 183
 QY 176 FTTITFRMGKCTYFNSGADGAEILLTTTSGMGNGLDIMLDVQOEYLPVWRDNEETPEY 235
 DB 184 FKVFETRYGKCYTFNSGOGPRPLKTKMGGTGNGLEIMLDIOQDEYLPVWGFTDETSFEA 243
 QY 236 GIRVOIHSOEPIIDOLIGVSGYOTFVSCQOQLSFLPPWGDCCSSASLNPYEPEP 295
 DB 244 GIKVQIHSODEPEIDQLGVAAGFOTFVSCOEORLITLPSWGTCNAVTMDSDP--- 299
 QY 296 SDPLGSPSPSPPTLTMGCRCLAEYRYARKGCRMYVMPGDVPVCSPOQYKNCAPAI 355
 DB 300 -----FDYSITACRIDCEYRYLVENNCNRMVHMPGAPYCTPEQYKECADPAL 348
 QY 356 DALLRKDS--CACPNPCASTRYAKELSMVRIPSRARAFIARLNSEAVIAENVLALDI 413
 DB 349 DFLVERDOECYCEMPCNLTFRYGEKLSNVKIPSKASAKYLAKKFNKSEQYIGENIIVLDI 408

QY 414 FFEALNVEFEOKKAYEMSELLDGGOMGLFIGASLTITLLEIDYLCFEYFRDKVLGYFM 473
 DB 409 FFEVLNVEFTEOKKAYEIMAGLLDGGOMGLFIGASLTITLLEIDYAYEYIKHRLC----- 464
 QY 474 NROHSQRHSSTNLDQGLSHRTQVPHLSLGRPPPPPC 512
 DB 465 RRGCKQKEAKRSSADKGA-----LSLDVYKRRHNP 495

Search completed: October 11, 2002, 07:23:43
 Job time : 69 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 11, 2002, 05:23:16 ; Search time 51 Seconds

(without alignments)
1000,460 Million cell updates/sec

Title: US-09-530-233-2
Perfect score: 2851
Sequence: 1 MKPTSGPEARQPSDIRVF.....CAVTKTSLASHRTCYLTQL 531

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2768.5	97.1	532	2 JE0091	testis sodium chan
2	419	14.7	625	2 S68434	FMRamide-activat
3	414.5	14.5	699	2 S29499	sodium channel pro
4	407.5	14.3	669	2 A49585	Na+ channel protei
5	406	14.2	548	2 T25401	hypothetical prote
6	398.5	14.0	650	2 A54065	sodium transport p
7	391.5	13.7	660	2 I51684	epithelial sodium
8	386	13.5	632	2 I51682	epithelial sodium
9	374.5	13.1	640	2 I51915	epithelial sodium
10	373	13.1	638	2 S41159	sodium transport p
11	372	13.0	630	2 D87739	protein T28F2.7 [i
12	372	13.0	630	2 T35144	hypothetical prote
13	356	12.5	724	2 T25700	mechanosensory pro
14	353	12.4	664	2 T20420	hypothetical prote
15	351	12.3	737	2 T16737	hypothetical prote
16	349	12.2	663	2 T25569	hypothetical prote
17	348	12.2	669	2 I64847	epithelial sodium
18	342.5	12.0	749	2 T29859	mechanosensory pro
19	341	12.0	649	2 T38204	epithelial amilorid
20	338	11.9	638	2 T37309	flr-1 protein - Ca
21	337.5	11.8	545	2 T34429	hypothetical prote
22	336	11.8	795	2 T34468	hypothetical prote
23	326.5	11.5	849	2 T19878	hypothetical prote
24	326.5	11.5	926	2 H88226	protein Ca1c4.5 [i
25	315.5	11.1	638	2 T39196	amiloride sensitiv
26	309	10.8	629	2 T2571	hypothetical prote
27	298	10.5	608	2 T25572	hypothetical prote
28	288.5	10.1	613	2 T28952	hypothetical prote
29	267	9.4	611	2 T20501	hypothetical prote

30	266.5	9.3	643	2 T21296	hypothetical prote
31	264.5	9.3	599	2 T15552	hypothetical prote
32	260	9.1	297	2 T25652	degenerin 1 (DEG-1
33	246	8.6	978	2 T16948	hypothetical prote
34	206.5	7.2	606	2 JW0054	amiloride-sensitiv
35	193.5	6.8	907	2 T27317	hypothetical prote
36	189.5	6.6	292	2 T29233	hypothetical prote
37	184	6.5	840	2 T21333	hypothetical prote
38	166.5	5.8	384	2 T19513	hypothetical prote
39	128.5	4.5	565	2 T29813	hypothetical prote
40	111	3.9	240	2 T25814	hypothetical prote
41	107	3.8	699	2 T09069	probable CAMP-resp
42	105.5	3.7	592	2 T34446	hypothetical prote
43	105.5	3.7	1819	2 T32008	hypothetical prote
44	105	3.7	2364	2 A56577	microtubule associ
45	104.5	3.7	434	2 A32132	phosphorylate hy

ALIGNMENTS

RESULT 1	JE0091	testis sodium channel 1 - human
C:Species: Homo sapiens (man)		
C>Date: 14-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000		
C:Accession: JE0091		
R:Shibasaki, K., Maruno, F.		
Biochem Biophys Res Commun. 245, 589-593, 1998		
A:Title: Molecular cloning of a DEG/ENAC sodium channel cDNA from human testis.		
A:Reference number: JE0091; MUID:980238685		
A:Accession: JE0091		
A:Molecule type: mRNA		
A:Residues: 1-532 <ISH>		
A:Cross-references: DBJ:AB010575; NID:g3097313; PIDN:BAA25897.1; PID:g3097314		
A:Experimental source: testis		
C:Keywords: glycoprotein; mitochondrion		
F:43-61,443-462/Region: hydrophobic		
F:175/Binding site: carbohydrate (Asn) (covalent) #status predicted		
Query Match	Score 2768.5; DB 2; Length 532;	
Best Local Similarity	97.1% Pred. No. 2.3e-214;	
Matches 516; Conservative 4; Mismatches 11; Indels 1; Gaps 1;		
QY 1 MKPTSGPEARQPSDIRVFASNCMHGLGHVFGPSLSLRGMAAAVVLVAFLVQV 60		
DB 1 MKPTSGPEARQPSDIRVFASNCMHGLGHVFGPSLSLRGMAAAVVLVAFLVQV 60		
QY 61 AERVRYRREHNOTALDERESHRLVPAYTLGNIINFLRSRLTPNDLHMAGSALLGLDPA 120		
DB 61 AERVRYRREHNOTALDERESHRLVPAYTLGNIINFLRSRLTPNDLHMAGSALLGLDPA 120		
QY 121 EHAFLRALGRPPAPPGFMPSPFDMAQLYARAGSLDMLDCRFRGPGCGENETTF 180		
DB 121 EHAFLRALGRPPAPPGFMPSPFDMAQLYARAGSLDMLDCRFRGPGCGENETTF 180		
QY 181 TRMGKCYTFNSGADGELLTTTRGSGNGIDIMLDVQOEYLPVMDNEETPEVIRVQ 240		
DB 181 TRMGKCYTFNSGADGELLTTTRGSGNGIDIMLDVQOEYLPVMDNEETPEVIRVQ 240		
QY 241 IHSQEEPPITIDGLGVSGYGFVSCQOQUSFLPPMGDCSSALNRYEPEPDPDG 300		
DB 241 IHSQEEPPITIDGLGVSGYGFVSCQOQUSFLPPMGDCSSALNRYEPEPDPDG 300		
QY 301 SPSPSPYITLMGRLACETRYVARKCGCRMYVMPGDPVCSPOQYKNCAPADAIL 359		
DB 301 SPSPSPYITLMGRLACETRYVARKCGCRMYVMPGDPVCSPOQYKNCAPADAIL 359		
QY 360 RUDSCACPNPCASTRYAKELSMWRIPSRRAARLAKLRSEYIAENVALDIFEEALN 419		
DB 360 RUDSCACPNPCASTRYAKELSMWRIPSRRAARLAKLRSEYIAENVALDIFEEALN 419		
QY 420 YEVVEQKKAYEMSELLGDIGGQGLFGASLLTLETLIDYLCVEFVDKVLGFWNNQHSQ 479		

Y bld dot

|||||
Db 421 YETVQKAKYKSESLGIGGOMGLFISGLTLEILDYLCFVRDVLGYFWMRHSQ 480
OY 480 RHSSNLLQEGISGHRTOVPHLSGPRPTPCATKTLASHRCYLVTOI 531
Db 481 RHSSNLLQEGISGHRTOVPHLSGPRPTPCATKTLASHRCYLVTOI 532
RESULT 2
S68434
FMRamide-activated sodium channel protein, amiloride-sensitive - brown garden snail
C:Species: Helix aspersa (brown garden snail)
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 24-Sep-1998
C:Accession: S68434
R:Lingueglia, E.; Champigny, G.; Lazdunski, M.; Barbry, P.
Nature 378, 730-733, 1995
A:Title: Cloning of the amiloride-sensitive FMRamide peptide-gated sodium channel.
A:Reference number: S68434; MUID:96107314
A:Accession: S68434
A:Molecule type: mRNA
A:Residues: 1-625 <LIM>
A:Cross-references: EMBL:X92113; NID:G1149510; PID:6205469; PID:G1149511
C:Keywords: glycoprotein; sodium channel; transmembrane protein
F:71-88/Domain: transmembrane #status predicted <TM1>
F:537-557/Domain: transmembrane #status predicted <TM2>
F:134,196,303,349,365,372,473/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 14.7%; Score 419; DB 2; Length 625;
Best Local Similarity 22.2%; Pred. No. 1.3e-25;
Matches 136; Conservative 99; Mismatches 191; Indels 186; Gaps 20;
OY 17 IRVFNASNCMHGLGHVFGPSLSLRGMAAAVLSVATFLYQVAERYVREFFHQTAL 76
Db 43 IAEILOSENAGIAKIVTSRD-TRKRVIMALLVIGTAATQLSLVRKYLQFOVELS 101
OY 77 DERESHRLVFAVTCINP-----LRR-----SRLLPNLHAGSALLGLDPAEHAFLRA 128
Db 102 EIKDMPQVQYBSVICNTEPISLRTIRMYFNESQNLITWL--RFICKFREQDSFMNS 159
OY 129 LGRPPAPGFMPSPTF--DMAQLVYRACHSLDMLDCRFRCQPGCFNETTITF-RMGK 185
Db 160 I-----RAFYENLQDADAKLSHNEEDLMHCRFRNELCHVSNFSFFGCAFN 207
OY 186 CYTENSAGDAELLTTTRGCGNGDMLDVOQEELP---VWPDNEETPEVGIROYI 241
Db 208 CFTFESG---QRLQMAHATGPENGSLIFSEYKDDPLPGYGVYFNDDNIIHLSAGVRVY 263
OY 242 HSQEPPIIDOLGLGVSGYOTFVSCQOQSLFLRPPMGDCSSASLN--PNTPEPSDPL 299
Db 264 HAPGMPSPVDHGDIDIPGYSSVGLKAILHTRLPYPGNCNTMDLNGIKOYK----- 316
OY 300 GSPSPSPPYTLMGCRACETRYVARKCGRMVYMPGDVP----- 340
Db 317 -----YTFRACDLOLCKORLIQRCGCKSSALP-EVBSYNAIFCGYIKQMOEIRN 365
OY 341 -----VCSPOQYKCAHPAIDAILRKD-----SCAPNDCASTR 374
Db 366 HSNEDHNSQSEEDRAFIPTPLACEEERQKN-----LNNDRYELISCGFOFCSEFS 416
OY 375 YAKELSWRIP-----SRAAFLARKLRSEYLA----- 405
Db 417 YLKSLSLYWPLFEYQLSAVERFEKQERQAGQNHMKTAVEYLELAKHPSOKHLARNDSH 476
OY 406 -----ENVLALDIFPEALNYETVEOKKAYEASELLDIG 440
Db 477 MDLLISYSLSSEKEMAKESDLIRQNNLRNLITLIEDLSVEYRQLPAYGLADLEADIGG 536
OY 441 QMGFLIGASLTLEILDYLCFVRDVLGYFWMR-----HSQRHS 482
Db 537 TLGLMGISVLTIMELIELVY-----RLTLGLVFNSEKGLRPGPTTVNNNNSNNHSQ-ST 590
OY 483 STNLLQEGLSH 494

Db 591 SQHQLNGYMDH 602
RESULT 3
S29499
sodium channel protein alpha chain, epithelial, amiloride-sensitive - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jun-2000
C:Accession: S29499; S43503; S29715; S41158
R:Lingueglia, E.; Voilley, N.; Waldmann, R.; Lazdunski, M.; Barbry, P.
FEBS Lett. 318, 95-99, 1993
A:Title: Expression cloning of an epithelial amiloride-sensitive Na(+) channel. A new
A:Reference number: S29499; MUID:93170495
A:Accession: S29499
A:Molecule type: mRNA
A:Residues: 1-699 <LIM>
A:Cross-references: EMBL:X70521; NID:9433909; PIDN:CAA49916.1; PID:9433910
R:Canessa, C.M.
Submitted to the EMBL Data Library, March 1994
A:Reference number: S43503
A:Accession: S43503
A:Molecule type: mRNA
A:Residues: 2-598, 'DV', 601-699 <CAN>
A:Cross-references: EMBL:X70497; NID:9458845; PIDN:CAA49905.1; PID:9458846
R:Canessa, C.M.; Horisberger, J.D.; Rossler, B.C.
Nature 361, 467-470, 1993
A:Title: Epithelial sodium channel related to proteins involved in neurodegeneration.
A:Reference number: S29715; MUID:93156815
A:Accession: S29715
A:Molecule type: mRNA
A:Residues: 2-194, 'P', 196-230, 'GAA', 234, 'LPAYATTI', 243-598, 'DV', 601-699 <CAN>
A:Cross-references: EMBL:X70497
R:Canessa, C.M.; Schild, L.; Buell, G.; Thorens, B.; Gautschi, I.; Horisberger, J.D.;
Nature 367, 463-467, 1994
A:Title: Amiloride-sensitive epithelial Na(+) channel is made of three homologous sub
A:Reference number: S41158; MUID:94150624
A:Contents: annotation
C:Superfamily: human amiloride-sensitive sodium channel protein; fibronectin type I r
C:Keywords: glycoprotein; sodium channel; transmembrane protein
F:110-152/Domain: transmembrane #status predicted <TM1>
F:422-457/Domain: fibronectin type I repeat homology <IFR>
F:567-613/Domain: transmembrane #status predicted <TM2>
F:423,539/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 14.5%; Score 414.5; DB 2; Length 699;
Best Local Similarity 22.9%; Pred. No. 3.4e-25;
Matches 147; Conservative 97; Mismatches 226; Indels 161; Gaps 21;
OY 6 GPE-EARRQPSD-----IRVFNASNCMHGLGHVFGPSLSLRGMAAAV 49
Db 58 GPEAPAPQPTTEERALLTFHRSYRELFOFCNNTTIGATRIIVCSKHNRMKTAFWA--- 114
OY 50 VLSVATFLYQVAERYVREF-HHOTALD-ERESRLVFAVTCINILRRSL----- 102
Db 115 VLWCTFGMMTYQFALIEEYLSYFVSINLINSUKLVFPVATCTLLPYYTEIKEELE 174
OY 103 -----TPNDLHAGSALLGLDPAEHAFLRAGRAPPGEMSPTFMAOLYARAG 154
Db 175 ELDRTEQTLFDLYKYNSYTRQAGARRRSSRDLLGAPPHLQRLRTPPPYSQRTASG 234
OY 155 HS----- 156
Db 235 SSSVVDNNPQVDRKDWKIGFOLCQNKSDCFYQYSSGVDAVREWRPHYINILSRLSDT 294
OY 157 -----LDMMLDCRRGRCPCGRENFTTFTTR-GKCYTFNSGADGAELTTTRGNG 207
Db 295 SPALKEEALGNFTTCRPNQANQANYSKPHHPYGCYTFND-KNNSNLSMMSMGVN 353
OY 208 NGDILMDVOOEELPYVRDNEETPEVGIROYIHSQEPPIIDOLGLGVSPGYOTFVSC 267
Db 354 NGLSLTLRTEQNDRIPL-----LSTYTGARVYVHGDQEPFMDQGFNLPFVETISIM 407
OY 268 QOQOOLSFLRPPMGDCSSASLNPNYEPSPDPLGSPSPSPPYTLMGCRACETRYVARK 327


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Db 299 KUKTTHY-----TGTYTVEACFRSCMQEKTIASCCG---YYPYSHASNT 340
Oy 345 QOYKNCAN-----PAIDAILRKDS-----CACPNPCASTRYAKELSVIRPSRA 388
Db 341 TQYVSDNCGVQTLNLCNCDLINSADSTFEDVLTQDCDQPCPEIDSYGVTVSTAOCPSPS 400
Oy 389 AARFLARKLN-----RSEA---YIAENVLALDIFEALNVEYBOKKAYEMSELL 435
Db 401 ---YVTECNPGPGSPGMPDASGESCLDMYKANTILIEIYERHNFQVLTPESPATFVNFI 457
Oy 436 GIGGOMGCFITASLITLIEILDYCEVFRDKVLGYFMNRQHSQRHSSTNLLOEGIGSHR 495
Db 458 SOVGGOVGFLEMTSIIISALE---YLVLPF---LVFEFYCTHKSRRAEIEOLEMDIKRAK 510
Oy 496 TOVPHLS 502
Db 511 DDVDOVA 517

```

RESULT 6

A54065 sodium transport protein gamma chain - rat

N:Alternate names: sodium channel protein KCNaCH2

C:Species: Rattus norvegicus (Norway rat)

C:Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jun-2000

C:Accession: A54065; S41160

R:Linqueglia, E.; Renard, S.; Waldmann, R.; Volley, N.; Champigny, G.; Plass, H.; Lazdu

J. Biol. Chem. 269, 13736-13739, 1994

A:Title: Different homologous subunits of the amiloride-sensitive Na(+) channel are diff

A:Reference number: A54065; MUID:94245676

A:Accession: A54065

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-650 <LIN>

A:Cross-references: GB:X78034; NID:9495270; PIDN:CAA54364.1; PID:9495271

R:Canessa, C.M.; Schild, L.; Buell, G.; Thorens, B.; Gautschi, I.; Horisberger, J.D.; Ro

Nature 367, 463-467, 1994

A:Title: Amiloride-sensitive epithelial Na(+) channel is made of three homologous subun

A:Reference number: S41158; MUID:94150624

A:Accession: S41160

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-52, 'P', 54-572, 'C', 574-650 <CAN>

A:Cross-references: EMBL:X77933; NID:9458849; PIDN:CAA54905.1; PID:9458850

C:Superfamily: human amiloride-sensitive sodium channel protein; fibronectin type I repe

F:373-408/Domain: fibronectin type I repeat homology <LFR>

Query Match 14.0%; Score 398.5; DB 2; Length 650;

Best Local Similarity 23.2%; Pred. No. 6.1e-24;

Matches 154; Conservative 93; Mismatches 233; Indels 183; Gaps 26;

```

Oy 3 PTSGPEEARROPSDRIVRASNSMGLGHVPGPSLSLRGMAAAYLVSAATFLYQVAE 62
Db 16 PVRGP-QAPPTIKDLNMWCMNTNTHGCRRIYVSRG-RLRRLLMFTFLTAVALLIWQCAL 73
Oy 63 RRVRYRREHHOTALDERESH-RLVFPATVLCINPLRHSR---LTPNDLMAGSALLG 116
Db 74 LV-----ESFYVSVSIVKHOKLDPRAVTICINIPKYKSANVSDLLDLDSE-TQALIS 127
Oy 117 LDPAEHAFLRALGRPA---PPGF---MSPPTFD-----MAQL-----Y 150
Db 128 LYGVESRRKRRRAGSMPTLEGTPRPFKFLPLVLFENENKGAARDFTGRKRKISKII 187
Oy 146 -----MAQL-----Y 150
Db 188 HKASVNVHVESKLVGFOLCSNDTSDCATYTFSSGINAIOEMYKLYHNTMAOYPLEKK 247
Oy 151 ARAGSLDMLDLCRFRGPOCGPENFTTIFTRM-GKCYTFNSGADGAEILLTTTRGGMNG 209
Db 248 INMSASABELLYTCFFDGDSCDARNFTLPHRPMYGCYTFNN-KENATILLISMGSGSEVG 306
Oy 210 LDMLDVQOEEYLPVWRDNETPFEV---GIRVOIHSQEEPIIDOLGLGVSPGYOTFVS 266

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Db 307 LOVILYINDEY-----NPFVLSSTGAKVLLHOOKEYPFIDVGMETIAMSTSIG 357
Oy 267 CQOQOOLFPPPMGDCSSASLNPVEPESDPLGSPSP---SPPYTLMGRLACERY 323
Db 358 MLTSEFKLSPEYSOCTED-----GSDVPTNTIYNNAYSIQITLYSCFQTK 403
Oy 324 VARKGCGRMVY--MPGDVPCSPQOYKN---CAHPAIDAILRKD---SCACPNCASTRY 375
Db 404 WVEKCGCAQYSGPLPPAANYCYQHHPMMYCYQYQAFVNEELGCGSVCKQSGSFHEW 463
Oy 376 AKELSVIRPSRAARFLA-----RKLNRSEAYIAENVLADIFEALNVEY 423
Db 464 TLTTSLAOWPSEASEKWLNLVLTWDSQOINKKLTDT-----LAKLIFYKDLNORSI 517
Oy 424 EOKKAYEMSELLGDIGGOMGCFITASLITLIEILDYCEVFRDKVLGYF----- 472
Db 518 MESPANSTIELMNSFGQGLGMLMSSCVVCEIIT---EVF---FIDFSIARQMHKA 570
Oy 473 ---WNROHSQRHSSTNLLOEGIGSHR---TQVPHLSIGPR-PPYPPCAVTKTSLASHRT 524
Db 571 KDMWARRQTPPETETPSSRQGDNPALDITDDELPTFTSAMRLPAPAGSVPTPPRYNT 630
Oy 525 CYL 527
Db 631 LRL 633

```

RESULT 7

I51684 epithelial sodium channel, gamma subunit - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jun-2000

C:Accession: I51684

R:Pnotti, A.; May, A.; Canessa, C.M.; Horisberger, J.

Am. J. Physiol. 269, 188-197, 1995

A:Title: The highly selective, low conductance epithelial sodium channel of Xenopus 1

A:Reference number: I51682

A:Accession: I51684

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-660 <PUD>

A:Cross-references: EMBL:U25342; NID:9886045; PIDN:AAA74972.1; PID:9886046

C:Genetics:

A:Gene: gammaXENAC

C:Superfamily: human amiloride-sensitive sodium channel protein; fibronectin type I r

F:375-410/Domain: fibronectin type I repeat homology <LFR>

Query Match 13.7%; Score 391.5; DB 2; Length 660;

Best Local Similarity 21.7%; Pred. No. 2.3e-23;

Matches 141; Conservative 105; Mismatches 232; Indels 171; Gaps 23;

```

Oy 3 PTSGPEEARROPSDRIVRASNSMGLGH-VFGPSLSLRGMAAAYLVSAATFLYQVA 61
Db 17 PVTGP-QAPTYELMQWCMNTNTHGCRRIYVSKG-RLRRWIMISLTLCAYVFWQCA 73
Oy 62 RRVRYRREHHOTALDERESHRLVFPATVLCINPLRHSRL-----TPNDLH 108
Db 74 LLIMSY---YVSASITTYFQKLVYPAVTICNLNPNYSISKYKDRALALEKETISQILNIY 130
Oy 109 WAGSALL-----GLDPAEHAFLRAL----- 129
Db 131 GFTPELLIRSKRDVGVNENSTFEDIFLKQIDPLRYLESVGSQLVVSDLTKKRTKMSAKVI 190
Oy 130 ---GRPPAPPGFM---PSPTFD-----MAQLYAR--- 152
Db 191 HRDAESVODPGNMWGFKLCDPRNSSDCITFTSSGVNAIOEMYRLHYNTLAKISMEDKI 250
Oy 153 -AGHSLDMLDLCRFRGPOCGPENFTTIFTRM-GKCYTFNSGADGAEILLTTTRGGMNG 210
Db 251 AMGYADELLIYTCFFDGDSCDARNFTLPHRPLYGICITYFN-AEAGNLLVSMGGAEGEL 309
Oy 211 DIMLDVQOEEYLPVWRDNETPFEV---GIRVOIHSQEEPIIDOLGLGVSPGYOTFVS 270

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[illegible]

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RESULT 8
151682      epithelial sodium channel alpha subunit - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jun-2000
C:Accession: J01682
R:Puoti, A.; May, A.; Canessa, C.M.; Horisberger, J.
Am. J. Physiol. 269, 188-197, 1995
A>Title: The highly selective, low conductance epithelial sodium channel of Xenopus laevis
A:Reference number: 151682
A:Accession: J01682
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-632 <PDB>
A:Cross-references: EMBL:U23535; NID:g968935; PIDN:AAY4970.1; PID:g968936
C:Gene(s):
C:Genetic(s):
A:Gene: alphaXENac
C:Superfamily: human amiloride-sensitive sodium channel protein; fibronectin type I repeat F:335-390/domain: fibronectin type I repeat homology <FI>

Query Match          13.5%, Score 386; DB 2; Length 632;
Best Local Similarity   21.5%; Pred. No. 5.9e-23;
Matches 135; Conservative 102; Mismatches 242; Indels 148; Gaps 23;

QY    20  FASNSGMHGIGVPEPGSLIRGMMAAAVIVLSATFLIQAVERRYRRREFHNGALD-E 78
     |||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db    26  FCSTNTTTCAGLRILVCSRRNRMKTAFAWLFLFTVGIMYWQFG--LLFGQYSYPVSINLN 83

QY    79  RESRLTFPPAVTLICNLNPILRSRTLPNDLH-----WASSALLGLDPADHA 123
     |::||||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db    84  VASDKLTFFPAVTVCITLNFTRYKAI-QNDIQELDKETORTLYELYKYNSTGVQGWIAPNNOR 142

QY    124 AFLRALGRP---PAPPG-----FMPSPPT 143
       |||
Db    143 VKRDAGRPLYLELTPSGSETHRVSRVIEEELGYKRREMNIIGFKLCNETGGDCYYQT 202

QY    144 -----FDMAQLYARA-----GHSLDDMLDCRFEGGPCGBPNFTTTTRM-G 184
       ::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db    203 SCVDAILREMYRPHYINIILARVPQEAIAIDGEOLENIIFACRFNEESCCTKANASSFHNAITYG 262

QY    185 KCYTENSNG-AADAELLTTRTGCMGNGLDIMLVQOGEYLCPVRDNDEERPFVEGITVOHS 243
     |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db    263 NCYTNNONOSDSNISWMSSMPIKNGKITLVLTTEGDHYIPLLSS-----VAGANVLVHG 316

QY    244 QEEPIIDLQIGAGVSPGYOTFEWSCQQOOISFLRPWGQC----SSASINPNYEPRSDPL 299
     :||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db    317 HKEPAFMDONGFNIPGWMTSISGMKKETLINRGKGXYSCDESIGSVADVKNLFQS----- 371

QY    300 GSPSPSPSPSPPTLMGCRIACESTRYVARCKCGCRMV---MPGDVPVCSPOOVKNCAPAID 356

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Db 372 -----YTEQVCARSCFOALMVARCGGAYFYFLSPQD-QYCDYNNKHKSMGCHYK 420
QY 357 AIL-----RKDSC--ACNPICASTRYAKELSKWIRIPSPAARFLARKUNSEAYIAENVLA 410
Db 421 LIIEFTSKLCCFTFKCRPCPLVSEQITLAGYSKMNPVSDOWVLIHTLSROYNTLDRGIA 480
QY 411-LDIFEEALNIEYEQOKKAYEMSELGDIIGOMELFIGASLITLLEILDICEVFRKVL 469
Db 481 KLNIFYEELNKTILDESPTIMAMULLSIGOWSLMGSSVLSEVLELVEIDPV---II 537
QY 470 G-----YFMNQRHOSRHSSTNLDEGLSHHTQVPHSLIGRRP-----TPPC 512
Db 538 GVMILLHRYTKKANEGEETVVPTRPAPAFDLQOVPHPILRGDLSORLSIVADITPP 597
QY 513 AVTK-----TL$A-----SHRTCY 526
Db 598 AYESLDRSVGTLSSRSSSMRSNRSY 624

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RESULT 9
151915
Epithelial sodium channel beta subunit - human
N:Alternate names: sodium channel, nonvoltage-gated 1, beta chain; sodium transport p
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 17-Nov-2000
C:Accession: 151915; 138203; A54986
R:McDonald, F.J.; Snyder, P.M.; Price, M.P.; Welsh, M.J.
Am. J. Physiol. 268, 1157-1163, 1995
A>Title: Cloning and expression of the beta and gamma subunits of the human epithelia
A:Accession: 151915
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-640 <RES>
A:Cross-References: GB:I36593; NID:g987622; PID:AAA75459.1; PID:g987623
R:Voilley, N.; Bassilana, F.; Mignon, C.; Merscher, S.; Mattei, M.G.; Carle, G.F.; Laz
Genomics 28, 560-565, 1995
A>Title: Cloning, chromosomal localization and physical linkage of the beta and gamma
A:Reference number: 138203; MUID:96039270
A:Accession: 138203
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-313, 'G', 315-335, 'A', 337-497, 'V', 499-640 <RES>
A:Cross-References: EMBL:X87159; NID:G1004270; PID:CAA60632.1; PID:g1004271
R:Shimkets, R.A.; Warner, D.G.; Bositis, C.M.; Nelson-Williams, C.; Hansson, J.H.; S
Cell 79, 407-414, 1994
A>Title: Liddle's syndrome: heritable human hypertension caused by mutations in the b
A:Reference number: A54986; MUID:95042738
A:Accession: A54986
A:Molecule type: DNA
A:Residues: 515-640 <SHI>
A:Cross-References: GB:U16023; NID:g563833; PID:AAA67036.1; PID:g563833
A>Note: authors translated the codon GTC for residue 630 as Thr, ATC for residue 631
C:Genetics:
A:Gene: beta hENaC; GDB:SCNN1B
A:Cross-References: GDB:434471; OMIM:600760
A:Map position: 16p12.2-16p12.1
C:Superfamily: human amiloride-sensitive sodium channel protein; fibronectin type I r

Query Match 13.1%; Score 374.5; DB 2; Length 640;
Best Local Similarity 22.1%; Pred. No. 5e-22;
Matches 131; Conservative 93; Mismatches 222; Indels 147; Gaps 22;

QY 20 FASNCSMGLGHVSPGSLISLRGMAAAVILSVATFLYQVAERYRYRREPHHOTALDER 79
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 29 YCDNTFTGHPKRIIDCG--PKKKAMFLTLFLTFLALVCMQGIKFTLTSWEVSYSIV- 85
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 80 ESHRTVFPAYVLCNTNPLRRSR- - - - -LTPNDLH- - - - -W 109
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 86 GFKTMDPFPVATVTCNAPSFKYSIKIKHLKDLDELMAEVLERILAPLASHANATRNUNSIW 145

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OY 110 AGSALLGLDP-----AEHAFLRALGRPPAP 136
| : | : |
DB 146 NHTPLVLIDERNPHVPLVDFGDHNGNLSSASEKICNAHCKMAMRLCSLNRQCF 205
OY 137 GFMSPPTDMDQVYARAGHSL-----DMLDCRRGOCPEPNTTIF 180
| : | : |
DB 206 RNFATATATLTEMVLIQATNIFAQVPOQELVEMSYRGEOMILACLEFGAEPNRYNFTSTIF 265
OY 181 -TRMKCTFENSGADGAEILLTTRGGMNGLDIMLDVOOEELPVRROHEEPFEVGTIV 239
| : | : |
DB 266 YPHYNCTIFNMGM-T-EKALPSANPTEFGLKLIDIGEDIVPPLAST-----AGVRL 318
OY 240 QIHSGEPPILDQLGVSPGYQTFVSCQOQOLSEFLPPWGDSSASLNPYEPEPSDPL 299
| : | : |
DB 319 MLHEGRSVPTFIDEIGIYPMSCFETSIGVLYDKLRMGEYSFC-----TYN----- 364
OY 300 GSPSP-----SPSPYTLMGCRCLACETRYVARKCCG-RMYV-MPGDVPVCSPOQYKNC 351
| : | : |
DB 365 GSEVFNQNFSDYNTYTSIOACLRSCEFODHMRNCNCGHYLPPLRGEKCYNNRDPDMA 424
OY 352 HPATD---AIIKRDSC--ACPNPCASTRYAKELSMVRIPSRAPARFLARKLNSE----- 401
| : | : |
DB 425 HCYSPLQMSVAMORETCIGMKESCNDTQKMTISMADMPSEASEDMIFRHVLSQERDOSTN 484
OY 402 -AYIAENVLALDIFFEALNYETVEOKKAYEMSELGIDIGOMGLFTIGASLTITILELDYL 460
| : | : |
DB 485 ILSRKGIYKLNIFFOEPRNRTIEESANNIYLLSLNGOGGCFMGMGSVLCLE----- 539
OY 461 CEVFDKVLGTFWNRHSHSSTNL-----LOEGLSHRTQVPHLSLGRPPT 509
| : | : |
DB 540 ---FGEIITDFW-----ITIKLVALKSLRORRAQSY--AGP-PPT 577

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RESULT 10

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S41159
sodium transport protein beta chain - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jun-2000
C:Accession: S41159
R:Caenessa, C.M.; Schild, L.; Buell, G.; Thorens, B.; Gautschi, I.; Holsberger, J.D.; RC
Nature 367, 463-467, 1994
A:Title: Amiloride-sensitive epithelial Na(+) channel is made of three homologous subun
A:Reference number: S41158; MUID:94150624
A:Accession: S41159
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-638 <CAN>
A:Cross-references: EMBL:X77932
C:Superfamily: human amiloride-sensitive sodium channel protein; fibronectin type I repe

```

```

Query Match 13.1%: Score 373; DB 2; Length 638;
Best Local Similarity 21.4%; Pred. No. 6.6e-22;
Matches 129; Conservative 100; Mismatches 223; Indels 140; Gaps 23;

```

```

OY 20 FASNCMHGLGHVFGPGLSLRGMMAAVALSVATFLYQVAERYRYREEHHQTALDER 79
| : | : |
DB 29 YCNNTNTGTPRIICEG--PKKKAMMFLTLFLACLVCMQGVETQIOTLSWEVSVL-SM 85
| : | : |
OY 80 ESHRLVPAVTLNINPLRBSR-----LTPRLDLH-----W 109
| : | : |
DB 86 GFKTNFPAVTVCSSPQYSKVHKHLKOLYKLMKLAVALDKLILAKSSHTNTSTLNTFTI 145
| : | : |
OY 110 AGSALLGLDP---AEHAFLRALG---RPPAPGF----- 138
| : | : |
DB 146 NHTPLVLIDERNPHVPLVLFQDSHNSNPAPSTCNAOGCKVAMRLCSANGVTCFRN 205
| : | : |
OY 139 MPSPFEDMAQLY-----ARAGSLDMLDLCRRGOCPEPNTTIF-T 181
| : | : |
DB 206 FTSATQATTEVYIIOATNIFSQVLPQDLVGMGYADRIILACLCTEPECSSHRNFTPIYP 265
| : | : |
OY 182 RMGCIYFNSGADGAEILLTTRGGMNGLDIMLDVOOEELPVRMRDNSETFEVCIRQOI 241
| : | : |
DB 266 DYGCYIFNMGM-T-EKALPSANPTEFGLKLIDIGEDIVPPLAST-----AGARLML 318

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OY 242 HSQEEPPILDQLGVSPGYQTFVSCQOQOLSEFLPPWGDSSASLNPYEPEPSDPLGS 301
| : | : |
DB 319 HQGRTPPIFREGIYAMAGTETISIGVLDKLOGKEPRTSPCTMNSDVALQVLYSD----- 374
OY 302 PSPSPSPYTLMGCRCLACETRYVARKCCG-RMYV-MPGDVPVCSPOQYKNCAPDAID--- 356
| : | : |
DB 375 ---NTYTSIOACLHSCFODHMRNCNCGHYLPPLRGEKCYNNRDPDMAVYCLSIOM 430
OY 357 ALLRQDSC--ACPNPCASTRYAKELSMVRIPSRAPARFLARKLNSE-----ATIAENV 408
| : | : |
DB 431 SVVORETCLSMKESCNDTQYKMTISMADWPSEASEDMILHVLQERDOSTNITLSRGI 490
OY 409 LALDIFFEALNYETVEOKKAYEMSELGIDIGOMGLFTIGASLTITILELDYLCEVFRDKV 468
| : | : |
DB 491 VKNLTYFOEPRNRTIEESANNIYLLSLNGOGGCFMGMGSVLCLE-----FGEIT 542
OY 469 LGYFNNRHSORHSSSTNLQ-----EGLSHRTQVPHLSLGRPPTPCAVTKTLSASHR 523
| : | : |
DB 543 IDFIW-----ITVILKVASCKGLRRRRQRPY--TGP-PPT-----VAELVEAHT 584
OY 524 TC 525
DB 585 NC 586

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RESULT 11

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protein T28F2.7 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: D87739
R:anonymus, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998

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A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bio
A:Reference number: A75000; MUID:99065613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C-
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
A:Accession: D87739
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-630 <STO>
A:Cross-references: GB:chr_I; PID:AB53057.1; PID:g2047351; GSPDB:GN00019; CESP:T28F
C:Genetics:
A:Gene: T28F2.7
A:Map position: 1

```

```

Query Match 13.0%: Score 372; DB 2; Length 630;
Best Local Similarity 25.1%; Pred. No. 7.8e-22;
Matches 145; Conservative 92; Mismatches 233; Indels 108; Gaps 26;

```

```

OY 1 MKPTGPREARROPDIRVFASNCMHGLGHVFGPGLSLRGMMAAVALSVATFLYQV 60
| : | : |
DB 12 LKPTS-----KRASQLIVDPVAHLKRIKITEGVSSITRSEHFSSKVMFSFESLYNA 65
| : | : |
OY 61 AERYVYREFFHQTALDERSH-----RLVPAVTLNINPLRBSRLTP-NDLHWAG 111
| : | : |
DB 66 TQ--QHVVVLNGYTVV--KDGHSVFLISEGGMQOPRVATVCSFNPIKRTVEALNSTKOLS 121
| : | : |
OY 112 SALLGLDPAEHAFLRALGRPPAP-----FEFMS-PTFEDMAQLYARAGSLDML 161
| : | : |
DB 122 DDLIDYLMFNSDAMTLGRADAASLHSGDNVFKIYVSSHNFATADNFMKAGFSCGMF 181
| : | : |
OY 162 LDCRPGOP---CGPENTTITFTRGKCYTFN-SGADAEILLTTRGGMNGLDIMLDVQ 217
| : | : |
DB 182 KMSFGGRFPDCC--KYATPIFSDLGKCFITLNLQSDSKSMKMKOTEPGIAAGLQIILDSH 239
| : | : |
OY 218 QEEYLPVRDNEE--TP-----FEVGIRVOHSQEEPPILDQLGVSPGYQTFVSCQO 269
| : | : |
DB 240 LEEQF---DSETDGVTVPFSSAFENGFRFYIHSSEELPLASGIAVSPSVVYALSS 295
| : | : |
OY 270 QQLSFLPP-PWGDCSSASLNPYEPEPSDPLGSPSPSPYTLMGCRCLACETRYVARKC 328
| : | : |

```

```

Db 296 SKYILLSSNAGNCSD-----SWPRGY---DYSGPYTSAMCSTMCKAQYFQNL 341
Qy 329 GCR-MY-----MPGDVPVCSPOQKNCANPAIDALILKRDSC-ACPNPCASIRYAK 377
Db 342 GCSPTSYNHLNRPNDCTPEYFICMDTKMKKYVNOSEN--IEMPTCECKVECKSOYHS 399
Qy 378 ELSMVAIPSRAAARFLARLNSEA----YIAENVLALDIFFEALNYETVEOKKAEMSE 433
Db 400 FMSYCGKLSRGALMLWT-LKQKQETWTIPMKLNPOVAVVFPFDMSTYETICKRGSLTE 458
Qy 434 LIGDGGGMLFTIGASLTITILEIDLYCEV---FROKVLGYFWNRQHSQ----- 479
Db 459 LLSDIGNGMGFMGMSVFTIIEFLFLSKIGWIGFSRKRDRDYSKKNNEHEKELEDY 518
Qy 480 -----RHST-----NLQOE---GLGSHRTQVPHSL 503
Db 519 VTGFKLFRHRKSGKDMSHLEKIKGLSMHRVYSEQLNV 556

```

RESULT 12

T15144

hypothetical protein T28F2.7 - Caenorhabditis elegans (fragment)

C.Species: Caenorhabditis elegans

C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C.Accession: T15144

R.Madsen, C.; Fronick, B.

submitted to the EMBL Data Library, April 1997

A.Description: The sequence of C. elegans cosmid T28F2.

A.Reference number: Z18300

A.Accession: T15144

A.Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: DNA

A.Residues: 1-630 <MAP>

A.Cross-references: EMBL:AF000198; NID:g2047345; PID:g2047351; PIDN:AA05057.1; GSPDB:GN

A.Experimental source: strain Bristol N2; clone T28F2

C.Genetics:

A:Gene: CESP:T28F2.7

A:Map position: 1

A:introns: 65/3; 83/3; 113/1; 174/2; 353/1; 430/2; 538/2

Query Match

Best Local Similarity 13.0%; Score 372; DB 2; Length 630;

Matches 145; Conservative 92; Mismatches 233; Indels 108; Gaps 26;

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Qy 1 MKPTSPPEARQPSDIRFPASCSMHGIGHVFGPSLSLRGMMAAVLVATFLYQY 60
Db 12 LKRF-----KRSQILIVDPYAHLRKIKNEGVSITRESEHPSKWFSEESLYNA 65
Qy 61 AERVRYREFHQTALDERESH-----RLVEPAVTLTCLNPLRSLRTP-NDLHMAG 111
Db 66 TQ-QHYWNLNGTYW--KDGHSFLSSGGMQFPRTYVCSFNPTRKTYEALNSTKDS 121
Qy 112 SALLGDPAEHAFLRAGRPAP-----PGFMPSP-PTFDMQLYARAGSHLDDML 161
Db 122 DDLDTLVLMFNSDAMTLGYGADAASLHSGDNVFKHYVSSHPNTAANFMDAFCSGDMF 181
Qy 162 LDCRFGRQ---CGPENFTTITRMGKCYTFN-SGADGAEELLTTTRGCMGNGLMDL 217
Db 182 KMSCFGRRPDCD--KYAATPFIISDLCKFTLNLQSGDKSMKMQTPEPIAGAIQIILDSH 239
Qy 218 OEELPLVWMDNEE--TP-----FEVGIROVHISOEPPILDQIGVSPGYQTFVSCQ 269
Db 240 LEEQF-----DSETDGVTPVFSASFENGFRFYIHSSEIPLFLASEGIAVSDSVYSLSS 295
Qy 270 QQLSFLPP-PMGDCSSASINPNYEPSPDPLGSPSPSPPTLMCRLACETRYVARK 328
Db 296 SKYILLSSNAGNCSD-----SWPRGY---DYSGPYTSAMCSTMCKAQYFQNL 341
Qy 329 GCR-MY-----MPGDVPVCSPOQKNCANPAIDALILKRDSC-ACPNPCASIRYAK 377
Db 342 GCSPTSYNHLNRPNDCTPEYFICMDTKMKKYVNOSEN--IEMPTCECKVECKSOYHS 399
Qy 378 ELSMVAIPSRAAARFLARLNSEA----YIAENVLALDIFFEALNYETVEOKKAEMSE 433

```

```

Db 400 FMSYCGKLSRGALMLWT-LKQKQETWTIPMKLNPOVAVVFPFDMSTYETICKRGSLTE 458
Qy 434 LIGDGGGMLFTIGASLTITILEIDLYCEV---FROKVLGYFWNRQHSQ----- 479
Db 459 LLSDIGNGMGFMGMSVFTIIEFLFLSKIGWIGFSRKRDRDYSKKNNEHEKELEDY 518
Qy 480 -----RHST-----NLQOE---GLGSHRTQVPHSL 503
Db 519 VTGFKLFRHRKSGKDMSHLEKIKGLSMHRVYSEQLNV 556

```

RESULT 13

T25700

mechanosensory protein 10 - Caenorhabditis elegans

C.Species: Caenorhabditis elegans

C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000

C.Accession: T25700; S42224

R.Fulton, B.

submitted to the EMBL Data Library, August 1996

A.Description: The sequence of C. elegans cosmid F16F9.

A.Reference number: Z20071

A.Accession: T25700

A.Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: DNA

A.Residues: 1-724 <FRU>

A.Cross-references: EMBL:U67956; PIDN:AA07694.1; GSPDB:GN00028; CESP:mec-10

A.Experimental source: strain Bristol N2; clone F16F9

N.Huang, M.; Chalfie, M.

Nature 367, 467-470, 1994

A.Title: Gene interactions affecting mechanosensory transduction in Caenorhabditis el

A.Reference number: S42224; MUID:94150625

A.Accession: S42224

A.Status: preliminary

A.Molecule type: mRNA

A.Residues: 1-724 <HUA>

A.Cross-references: EMBL:L25312; NID:g414798; PIDN:AA017404.1; PID:g414799

C.Genetics:

A:Gene: mec-10

A:Map position: X

A:introns: 90/2; 121/2; 162/1; 189/3; 288/3; 312/1; 337/3; 368/3; 396/2; 421/2; 455/1

Query Match

Best Local Similarity 12.5%; Score 356; DB 2; Length 724;

Matches 138; Conservative 82; Mismatches 205; Indels 240; Gaps 22;

```

Qy 17 IRVFASCSMHGIGHVFGPSLSLRGMMAAVLVATFLYQYAVRVRYYREFHQTAL 76
Db 97 LQFCYKTTSHGI-PMUGQAPNSLYRAAWFLLICAQFINQAVAVIQYQKMDITDI 155
Qy 77 DERESHRLVPAVTLTCLNPLRSLRTPNDLHWAGSALLGL----- 117
Db 156 -QLKFTAPFPATLTCLNLNPKYKDSVIRSHD---SISKILGVFESVKKAGDSSSEALEEB 211
Qy 118 -----DPA----- 120
Db 212 EETEVYMGITTOAKRRKRGAGEKGFEPANSAECEDDEGSECEBERSTKPSGNDMC 271
Qy 121 ----- 120
Db 272 ICAFDQOTNDAMPCHRKEDQNTTTCQDCEHYLCSKAKKGTFRSELKKEPCIESKGLF 331
Qy 121 -----EHAFL-----RALGRPPAPPGF----- 138
Db 332 CIKHEHAAMVNLMEYFGDSEDFSEISTEEREL-----GFGNMTDEVAIVTKAKENI 384
Qy 139 ---MSPTEFMAQLVYARAGSHLDDMLDCRFGRQPCG-PENFTTIP-TRMGKCYTFNSGA 193
Db 385 IFMMSALSEQRILMSQAKHNL---IHKCSFNKPCDDIDQDFELVADPTFGKCFVNH-- 439
Qy 194 DGAELLTTTRGCMGNGLMDLMDVQOEYLVYWRDNEETPEFVGIRVOIHISOEPPILDOL 253
Db 440 DREIFRSSVAGQYQYGLRVMLFVNASDYLP-----TSAVGIIRLTIDHKDFPPDF 492

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```

Oy 254 GLVSPGVQTFVSCGOOOLFLPRPMDCSSASLNPNEPBDPLGSPSPSPPTLM 313
      |||:::|||||
Db 493 GYSAPTGYISFGGRMKMKMSLRAPYDDCEDATSNYTK-----GYATSE 540
      |||:::|||||
Oy 314 GCRLACETRYVARKCGGRWYMP--GDVPYCS--POQKNCAPH--AIDAILRRDSCAC 366
      |||:::|||||
Db 541 GCYPTCFEOLLIDRCGSDRFPFSIGGVPCQVFNKNHRECLEKHTHQEIGHSGFKHC 600
      |||:::|||||
Oy 367 PNPASTRYAKELSMVNPISRAARFL-----ARKLNSEAVTAENVLALDIFPEALNY 420
      |||:::|||||
Db 601 QQPENQITTYTSYSEAIWPSQALNISIGCEKEKAEBCN--EEY-KENAAMLEVFEALWF 657
      |||:::|||||
Oy 421 ETVBOKRAYEMSELLDIGGOMGLFEGASLLTTLLEILDYCEVFR--DKVLGYFNNRQHS 478
      |||:::|||||
Db 658 EYLSSEAYGYIKMMADFGCHLIGMSGVMTCE--FVCLAFELITYMAIHHIINQRI 714
      |||:::|||||
Oy 479 ORHSS 483
      |||:::
Db 715 RRREN 719

```

RESULT 14

T20420

hypothetical protein E02H4.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000

C:Accession: T20420

R:Barlow, K.

submitted to the EMBL Data Library, November 1995

A:Reference number: Z19273

A:Accession: T20420

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-664 <MIL>

A:Cross-references: EMBL:Z66003; PTDN:CAA91975.1; GSPDB:GN00028; CESP:E02H4.1

A:Gene: CESP:E02H4.1

A:Experimental source: clone E02H4

A:Position: x

A:Introns: 57/3; 102/3; 135/3; 166/1; 191/1; 221/2; 254/3; 314/2; 355/2; 386/1; 472/3; 5

C:Superfamily: human amiloride-sensitive sodium channel protein; fibronectin type I repeat

Query Match 12.4%; Score 353; DB 2; Length 664;

Best Local Similarity 25.7%; Pred. No. 1.8e-20;

Matches 98; Conservative 61; Mismatches 145; Indels 77; Gaps 13;

QY 148 QLYRAGHSIDMDLDCFRQPCGPENFTTIF-----TRNGKCYTENSADGAEELLTTT 202

Db 325 QRRALGIGKSELIKMCSFNGQOC---NIDTEFKLHIDPSFGNCYTEN--ANPEKKLASS 379

QY 203 RGGGNGNGDINDLMDQOEELFLPWRHNETPREVGIRVQIHSEEPRIIDQGLGVSPGY 262

Db 380 RAGSYGRLMFEVNSSDYL-----TTATGVRILHKECECPPEPTPTGYPAPTGV 432

QY 263 TVFSQCOQDLSEFLPPWGDG-----SSASLNPVNEPEPSDPLGSPSPSPPYTLMGCR 316

Db 433 SSFGISLAINIRLDPQVYNCLOKDNQPSRSIYKGVKYE-----GCF 475

QY 317 LACETRYAARCGCGRMVYMGDVPVCSFOYK-----NCAHPAIDAILRKS 363

Db 476 RSCYQYRIIAKGC-----ADPRYPKPKWRKSMCDSTWTTTLNCLTTEGAKLSTKEN 527

QY 364 ---CACRPACASTRYAKELSMVRIPSRAAAEFLARKLNRSAIYAENVLALDIFFEALNTY 420

Db 528 QKHCKCIOPCOODYTTTYSAAKMPGSGSIQTSNDHNSKDCNSYREHAMAEIYEOWSY 587

QY 421 ETVOKKAYESELLDGIQGGMGFLIGASLTLTLEILDYCEVRDKYGVF-----WNR 475

Db 588 EILHESEYSYFNLMADGGAGFLGASIMSVIEFL-----FFAVKTLGIACKPRRW-R 641

QY 476 QHSO---RHSSNTLQEGLSH 494

DB 642 OKTELLRAEELNDAEKGVSTN 662

RESULT 15

T16737

hypothetical protein R13A1.4 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T16737

R:Du. 2.

submitted to the EMBL Data Library, November 1995

A:Description: The sequence of *C. elegans* cosmid R13A1.

A:Reference number: Z18569

A:Accession: T16737

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-737 <DUZ>

A:Cross-references: EMBL:U04798; NID:g1065928; PID:g1065929; PIDN:AAA81473.1; CESP:R13A1

C:Genetics:

A:Gene: CESP:R13A1.4

A:Introns: 30/3; 80/2; 128/1; 155/3; 186/2; 232/3; 261/3; 307/3; 341/3; 394/2; 428/1;

Query Match	12.38:	Score 351:	DB 2:	Length 737:
Best Local Similarity	19.78:	Pred. No. 4.6e-20:		
Matches 144:	Conservative 19:	Mismatches 222:	Indels 276:	Gaps 26:
Qy	4	TSGPEARROPSDINV-----FASNCSMGHGIV----	FGPGSLSTRGMAAAY	49
Db	42	TSSRSLRSQADIDYTTTIKSLMPDFCARSTSHGIPVATISFFG-----RYWMAALF	94	
Qy	50	VLSVAFTLYQVAERVRYREFHHQTALD-ERESHRLVPATVLCININLRSRLT-----	103	
Db	95	MCMLAFLLQTYWTVSELYQ--RTIEMQLQFEAAAPATVCLNLFKXSELTQVEEI	152	
Qy	104	-----	103	
Db	153	KEGEDYWERVINARMMSDSMKPGGDILEAIVRKKRKSRLQLFPIDDEBLEGAYIOPV	212	
Qy	104	-----PN-----DLH-----AGSALLGLD	118	
Db	213	FVRCQCMMEQCVPRNRNLEVNASICMCFEDVTGRLLIPCYPTSVWTKKSGSISNTC	272	
Qy	119	P-----AEHAALRAL-----GRPPAPPGF	138	
Db	273	PDPDGPNAKQIAKHNSPLCLCOSISHHCWHPKDEIRMMNPNUNTYVSYTEPTEIT	332	
Qy	139	MSPTFDMAOL-----YRAGSHSLDDMLDCRFPGORCP	173	
Db	333	ETEEAFGSLDKDAGAITTQTKENLIFLYAALPRETRNLSYTLNEFYLRKSFNSKDCSM	392	
Qy	174	ENFTTIFT--RMGKCYTPNSGADGAELLTTTRGGGNGNGLDMLDVQOEYLPVRNDNEET	231	
Db	393	ERDFGLHVDPEYGCNYTFENFN-DSVE-LKNSRAGPMGLRLLLVNHQSDYMP-----T	443	
Qy	232	PEFVGIRQVHISOEPRPIIDQLGLCVSPGYOTFVPSQOOQLSFLPRPGDCSSA-----	285	
Db	444	TEAAGVRLVWEHODQDEPRDFFGYSAPRGFLSSFGLKTELKRLHRSAPGNCSDFFRPVRY	503	
Qy	286	SLNRPYDEPSPDLGSPSPSPSPRYTLLMGCLACETRYVARKCGRMVWGDVPCSP-	344	
Db	504	LYNEHYSE-----GCHRNCFOLKVLLEICG-----GDRFRPLPS	538	
Qy	345	QOQYKNC-AHPAID-----AILRKDS-----CACPNPCASTRYAKELSNVRIPSR--	387	
Db	539	EEHHRCKNKSXIDHQCLNSLSDSGGVYHHLHEQCEQRCPHEKVFETRYASASAMPQNFK	598	
Qy	388	--AAARFLAKLNSEA---YIAENVALDIFFEALNLEYEQKAYEMSELLDIGQM	442	
Db	599	IGTDCPAVSDIFNDTEACTEYRONTAYIIEIYEQLNFESELEKTAGATLVMLFSDFGNI	658	
Qy	443	GLTFGASLLTLELLDYICEYFR---DKVLGYPNNRQHSQNSHTNLLQBELSGHRQVP	499	
Db	659	GLWIGFVITAEAEAELECEICKLMTFGRGIYVQKKMGKGTSSSLM-----HID	709	

OY 500 HLSIGRPPTP 510
| | : |
Db 710 FLGRSPKXSP 720

Search completed: October 11, 2002, 07:27:27
Job time : 56 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2002, 04:20:18 ; Search time 35 Seconds

(without alignments)
587.431 Million cell updates/sec

Title: US-09-530-233-2
Perfect score: 2851
Sequence: 1 MKPTSGPEARQPSDINVF.....CAVKTLSASHRTCYLYTQL 531

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: **SwissProt 40**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1369	40.0	512	1	BNAL_RAT
2	1365	47.9	512	1	Q16515 homo sapien
3	1329	46.6	526	1	P55926 rattus norv
4	1298	45.5	574	1	BNM2_HUMAN
5	420.5	14.7	699	1	SCAA_MOUSE
6	419	14.7	625	1	PANA_HELAS
7	417	14.6	646	1	SCB2_XENLA
8	415.5	14.6	647	1	SCAB_XENLA
9	414.5	14.5	698	1	SCAA_RAT
10	407.5	14.3	669	1	SCAA_HUMAN
11	400	14.0	650	1	SCAA_BOVIN
12	398.5	14.0	650	1	SCAG_RAT
13	392	13.7	640	1	SCAA_RABIT
14	391.5	13.7	660	1	SCAG_XENLA
15	391	13.7	655	1	SCAG_MOUSE
16	386	13.5	632	1	SCAA_XENLA
17	384	13.5	653	1	SCAG_RABIT
18	383	13.4	637	1	SCAA_CHICK
19	381	13.4	663	1	SCG2_XENLA
20	379	13.3	641	1	SCAB_RABIT
21	375	13.2	638	1	SCAB_MOUSE
22	373.5	13.1	640	1	SCAB_HUMAN
23	372	13.0	638	1	SCAB_RAT
24	356	12.5	724	1	ME10_CAEEL
25	353	12.4	664	1	DEU1_CAEEL
26	351	12.3	777	1	UNCB_CAEEL
27	346	12.1	649	1	SCAG_HUMAN
28	342.5	12.0	768	1	MEC4_CAEEL
29	337.5	11.8	545	1	DEGM_CAEEL
30	336	11.8	795	1	DEG2_CAEEL
31	335.5	11.8	769	1	MEC4_CAEEL
32	326.5	11.5	849	1	DEG3_CAEEL
33	320.5	11.2	638	1	SCAD_PANTR

34	315.5	11.1	638	1	SCAD_HUMAN	P51172 homo sapien
35	310.5	10.9	273	1	SCAB_RANCA	O9w754 rana caesh
36	309	10.8	778	1	DEB1_CAEEL	P24585 caenorhabd
37	246	8.6	978	1	YSX7_CAEEL	Q10025 caenorhabd
38	107	3.8	699	1	ATPB_MOUSE	O35451 mus musculu
39	105	3.7	2459	1	MABP_RAT	P15205 rattus norv
40	104.5	3.7	433	1	ENO4_ANAPL	P19140 anas platyr
41	103	3.6	1739	1	CHD2_HUMAN	O14647 homo sapien
42	102.5	3.6	433	1	ENO4_CHICK	P51813 gallus gall
43	100.5	3.5	2476	1	ZAN_PIG	Q28983 sus scrofa
44	100	3.5	1403	1	CIC_DROME	Q9u1h0 drosophila
45	98.5	3.5	433	1	ENO4_TRASC	O9w711 tracheys s

ALIGNMENTS

RESULT 1	ID	BNAL_RAT	STANDARD:	PRT:	512 AA.
AC	BNAL_RAT	062362;			
DT	01-NOV-1997 (Rel. 35, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	01-MAR-2002 (Rel. 41, Last annotation update)				
DE	Amiloride-sensitive brain sodium channel BNAC1 (Amiloride-sensitive cation channel neuronal 1) (BNAC1) (Degenerin channel MDEG).				
GN	ACCNT OR BNAC1 OR MDEG.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.				
OX	NCBI_Taxid=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain;				
RX	MEDLINE=96209957; PubMed=8631835;				
RA	Waldmann R., Champigny G., Voilley N., Lazdunski M.;				
RT	"The mammalian degenerin MDEG, an amiloride-sensitive cation channel activated by mutations causing neurodegeneration in Caenorhabditis elegans."				
RL	J. Biol. Chem. 271:10433-10436(1996).				
CC	FUNCTION: NON-VOLTAGE-GATED AMILORIDE-SENSITIVE CATION CHANNEL PERMEABLE FOR SODIUM, POTASSIUM AND LITHIUM.				
CC	- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	- TISSUE SPECIFICITY: BRAIN AND NEURONS.				
CC	- DEVELOPMENTAL STAGE: APPEARS JUST BEFORE BIRTH, REACHES MAXIMUM LEVELS AFTER BIRTH, THEN DECLINES SLIGHTLY UNTIL ADULTHOOD.				
CC	- SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNELS FAMILY.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch).				
CC	EMBL: U53211; AAC52588.1; -				
DR	InterPro: IPR001873; ASC.				
DR	Pfam: PF00858; ASC. 1.				
DR	PROSITE: PS01206; ASC. 1.				
KW	Ionc channel; Transmembrane; Ion transport; Glycoprotein.				
FT	DOMAIN 1 37				
FT	TRANSMEM 38 58				
FT	DOMAIN 59 427				
FT	TRANSMEM 428 448				
FT	DOMAIN 449 512				
FT	DOMAIN 469 472				
FT	CARBOHYD 365 365				
FT	CARBOHYD 392 392				
FT	MUTAGEN 430 430				
FT	MUTAGEN 430 430				
FT	MUTAGEN 430 430				

CAUSING CELL DEATH.
S->E. INACTIVATION OF BNAC1 G(430)F.

FT	MUTAGEN	443	443	57739	MM:	380A0A77C3C430B03	CRC64:
SO	SEQUENCE	512	AA:	57739	MM:	380A0A77C3C430B03	CRC64:

Query Match {48.0%} Score 1369; DB 1; Length 512;
Best Local Similarity 50.8%; Pred. No. 7.7e-103;
Matches 256; Conservative 82; Mismatches 140; Indels 26; Gaps 5;

```

Oy 7 PEARARQSDIRIVFASNSCMHGLGVFPGGSLSLRGMAAVALVSLVATFLYQVAREVY 66
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 7 PSEGSLQPSLSQIFANTSTLHGRIHFYGPGLTIRRVMAVAFVSLGLLVESSRVSAY 66
Oy 67 YREFHQAFLARESHRLVFPVATTCNINPLRSRSTPTMDLHWAGSALLGLD-----PAE 121
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 67 YFSYCHVTKVDEYVAQSLVFPVATTCNINLGFPSRLTMDLTHAGELLALLVYNQIDPP 126
Oy 122 HAA---FLRALGPRPAPPGFMPSPTFDMAQLYARAGHSLDMLDLCRFRGQPCGGENFTT 178
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 127 HLAADPTVLEALHQKANPFRHYKPK-QFSMLEFLHRYGHDLCKMMLCKCFKGGCGHQDFTT 185
Oy 179 IFTFRGKCYTFENSGADGAEELTTTGGMGNGLDIMLVQOEERYLFWARDNEETPREVGIR 238
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 186 VFTKRGKCYMFENSGEDGKPLLTVYKGGTNGLEIMLIDQODEYLYLWGTETEEETFEAGVK 245
Oy 239 VOIHQOEERPIIDGLGLSVSGYOFVFGVCGQQOQLSEFLRPMDCSSASLNPVYEEPEPSP 298
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 246 VOIHQOEERPIIDGLGLSVSGYOFVFGVCGQQOQLSEFLRPMDCSSASLNPVYEEPEPSP 298
Oy 299 LGSPPSPSPPTLGLGCRACLETFRVARKCGGRMYMPGADVCSPOQKNCANPAIDAI 358
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 299 -----FPYISTACRIDCETRIIVENCRCRWYHMGDAPFCFPEQKCEAEFALGIL 350
Oy 359 LRKDS--CACPNPCASTRAKELSMWRIPSRAAARFLARKLNRSAYIAENYALDIFEE 416
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 351 AEKDSNYLCRTPCNLTRYKNELSMWKIPSKTSAKYLEKKFKSKSEYISENTIVDIFPE 410
Oy 417 ALNLTVYQKRAKAESESLLDGIGGGMGLFPGASLTILTEILDYLCDFVPDKVLGFWMRQ 476
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 411 ALNLTETIQKRAEYVAALDIDGGMGLFPGASLTILTEILFEDYIYELIKELKLLDGLKEE 470
Oy 477 HSQRHSSTNLQEGLSGHRTQVPH 500
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 471 EEGSHDENKSTCTDTPMHSRTISH 494

RESULT 2
BNAC1_HUMAN STANDARD: PRT: 512 AA.
ID BNAC1_HUMAN STANDARD: PRT: 512 AA.
AC Q16515; Q13553;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Amiloride-sensitive brain sodium channel BNAC1 (Amiloride-sensitive cation channel neuronal 1) (BNAC1) (Degenerin channel MDEC).
DE ACN1 OR BNAC1 OR ACN1 OR MDEC.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96209957; PubMed=8631835;
RA Waldman R., Champigny G., Voilley N., Lauritzen I., Lazdunski M.;
RT "The mammalian degenerin MDEC, an amiloride-sensitive cation channel activated by mutations causing neurodegeneration in Caenorhabditis elegans."
RT J. Biol. Chem. 271:10433-10436(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96215169; PubMed=8626462;
RA Price M.P., Snyder P.M., Welsh M.J.;

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RT "Cloning and expression of a novel human brain Na⁺ channel.";
 RL J. Biol. Chem. 271:7879-7882(1996).
 [3]
 RN SEQUENCE FROM N.A.
 RP TISSUE-Frontal cortex;
 RC MEDLINE-97188490; PubMed-9037075;
 RA Garcia-Anoveros J., Derfler B.H., Neville-Golden J., Hyman B.T.,
 RT Corey D.P.;
 RT "BNaCl and BNaC constitute a new family of human neuronal sodium
 channels related to degenerins and epithelial sodium channels.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:1459-1464(1997).
 CC -1- FUNCTION: NON-VOLTAGE-GATED AMILORIDE-SENSITIVE CATION CHANNEL
 CC PERMEABLE FOR SODIUM, POTASSIUM AND LITHIUM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: BRAIN AND SPINAL CORD.
 CC -1- SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNELS
 CC FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U53212; AAC50498.1; -;
 DR EMBL; U50352; AAC50432.1; -;
 DR EMBL; U57352; AAB49182.1; -;
 DR MIM; 601784; -;
 DR InterPro; IPR001873; ASC.
 DR Pfam; PF00856; ASC; 1.
 DR PROSITE; PS01206; ASC; 1.
 KW Ionic channel; Transmembrane; Ion transport; Glycoprotein.
 FT DOMAIN 1 37
 FT TRANSEM 38 58
 FT DOMAIN 59 427
 FT TRANSEM 428 448
 FT DOMAIN 449 512
 FT CARBOHYD 365 365
 FT CARBOHYD 392 392
 FT CONFLICT 495 495 T -> A (IN REF. 2).
 FT SEQUENCE 512 AA; 57709 MW; 7C95B0B32EF2814 CMC64;
 Query Match 47.9%; Score 1365; DB 1; Length 512;
 Best Local Similarity 50.6%; Pred. No. 1.6e-102;
 Matches 255; Conservative 83; Mismatches 140; Indels 26; Gaps 5;
 QY 7 PEARRRPDSIRIVRANSCSMGLGHVEFPGSLIRGMAAANVLSVATFLYQVAERRY 66
 DB 7 PSESLPSLOIRIIFAMNSTLHGIRIIFVYGLTIRRVLAAMAAVFGSLDLLLVESSEVS 66
 QY YREHHOTALDERSHRLVPAVTLCTNPLRBSRLTPNDLHMAGSALLGD-----PAE 121
 DB YFSYQHTATKDEYVAQSLVPAVTLCTNGLRFRSLTINDLYHAGELLALLDYNLIQIDP 126
 QY 122 HAA---FLRALGRPPAPGFMPSPTFMAQLYARAGSLDMLDRCRPGPCGPEFTT 178
 DB 127 HLAAPSVLEALRQKAFNFKRK-QFSMLLEFLHRGHDLMKMLATCKRGQEGCHQDPTT 185
 QY 179 IETRMGKCYTFNNSGADGAEILLTTRRGCGNGSLDMLDYOQEBEYLVPRWDNEETPREVGIR 238
 DB 186 VFTYKKGCKMYNSEDGCKPLLTYYKGGCGNLEIEMLDIOQDEYLPRIWGETEETFEAGVC 245
 QY 239 VOHSQSEPRPIIDGLGVSPGYQTFVSCQOQQLSFLPRPPGDCSSALNNYEPESDP 298
 DB 246 VOHSQSEPRPIIDGLGVSPGYQTFVSCQOQQLSFLPRPPGDCSSALNNYEPESDP 298
 QY 299 LGSPPSPSPYTLTMCGLACETRYVARKCCGRMYVMGADVPCSPQOYKCAHPAIDAI 358
 DB 299 -----FPYVSTTACRIDCETRIYENCNCRWYHMGDAPFCTPREHKKCAERALGL 350
 QY 359 LRKDS--CACPNPCASTRYAKELSMVRIPSRNAARFLARKLNRESEAYIAENVLADIFFE 416


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DR EMBL: U78181; AAB48981.1; -.
DR MIM: 602866; -.
DR InterPro: IPR001873; ASC.
DR Pfam: PF00858; ASC; 2.
DR PROSITE: PS01206; ASC; 1.
KW Ionic channel; Transmembrane; Ion transport; Glycoprotein;
KW Alternative splicing.
FT DOMAIN 1 44 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 45 65 POTENTIAL.
FT DOMAIN 66 476 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 477 497 POTENTIAL.
FT DOMAIN 498 574 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 368 368 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPIC 434 479 MISSING (IN ISOCFORM 2).
SQ SEQUENCE 574 AA; 64841 MW; 8A981ABD1488C03A CRC64;

Query Match 45.5%; Score 1298; DB 1; Length 574;
Best Local Similarity 45.7%; Pred. No. 4.7e-97;
Matches 258; Conservative 78; Mismatches 129; Indels 100; Gaps 9;

QY 13 QPDSIVFVNSCMHGLGHVFGPGLSLRRGMAAANVSVATFLVQARVRYRFRFH 72
DB 14 QPVSIGAFSSSTLHGIAHFEYERLSLKRALALCEFLGLAVLVCVTERVOYEFHYH 73
QY 73 QPALDERSHRLVPAVTLNINPLRRSRLLPDLHWAGS--ALLG----- 116
DB 74 VTRLEVAASQLTFPAVTLNLEFRFSQSKNDIYHAGELLALLNNRYEIPDTQMADEK 133
QY 117 -LDPAAHAFLRALGRPPAPGFMSPPTDMAOLYARAGHSLDDMLDCFRQPCGPE 175
DB 134 QLEIILDDKNFRS-----FKPR-FMREFYDRAGHDIDMLSCHFREGEVSAED 183
QY 176 FTFITFMKCYFENGSGADCAELLTTTRGSGMGLDMLDVOOEYLVPRDNEETFEV 235
DB 184 EKVFTRFKCKTFFNSGRDRPRLKTKMDGTGNGLEIMLDIDDEYLPVGETDETSFEA 243
QY 236 GIKVQIHSGEPPRIIDGLGVSPGYQTFVSCQOOLSELPWPWGSSASLNPTEPPE 295
DB 244 GIKVQIHSGDEPFIQDLGFGVAPGQTFVACQEQRLIYLPWPWGCKAVTMSDIDF 303
QY 296 SDPLGSPSPSPRYTLNLCRLACETRYVARKGCGRMVYPCGVPVCSPOQYRNCAPAI 335
DB 304 S-----YSITACRIDCEITRYLVENCNCRMHVHPGAPRCPQYRECCDPAL 350
QY 356 DALIRKDS--CACPNPCASTRYAKELSMVRIPIRAARFLARKLNSEAYIAENVLADI 413
DB 351 DFLVEYDQECYCEMPCNLTTRYKELSMVKIPKASAKYLAKEFKNSQOYIGENIYLDI 410
QY 414 FFEALNYETVEOKKAYEMSEL----- 434
DB 411 FFEVLNYETIEOKKAYEIGLGLLELMTPEVPSCHGHGVAPYHPKAGCSLLSHEGPPQR 470
QY 435 -----LGDIGGOMGLFGASLITLLELDYICEVFRKVLGYFMNRRQSHSTNLL 487
DB 471 PEPPCCCLDDIGOMGLFGASLITLLELDYAVEYIKRKLCL---RKGCKQEARSSA 526
QY 488 QEGLSHRTQVPHLSLGPRTPTPPC 512
DB 527 DKGVA-----LSLDVYKRHNPC 543

RESULT 5
SCAA_MOUSE STANDARD: PRT: 699 AA.
AC 061180: Q9WU37;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Amloride-sensitive sodium channel alpha-subunit (Epithelial Na+
DE channel alpha subunit) (Alpha ENaC) (Nonvoltage-gated sodium channel
DE 1 alpha subunit) (SCN5A) (Alpha NaCh).
GN SCN5A.

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Kidney;
RX MEDLINE=99345762; PubMed=10409305;
RA Ahn Y.J., Brooker D.R., Kosari F., Harte B.J., Li J., Mackler S.A.,
RA Kleyman T.R.;
RT "Cloning and functional expression of the mouse epithelial sodium
RT channel.";
RL Am. J. Physiol. 277:F121-F129(1999).
RN [2]
RP SEQUENCE OF 445-558 FROM N.A.
RC STRAIN=CD-1; TISSUE=Kidney;
RX MEDLINE=97428085; PubMed=9284273;
RA Dagenais A., Kothary R., Berthiaume Y.;
RT "The alpha subunit of the epithelial sodium channel in the mouse:
RT developmental regulation of its expression.";
RL Pediatr. Res. 42:327-334(1997).
CC - FUNCTION: SODIUM PERMEABLE NON-VOLTAGE-SENSITIVE ION CHANNEL.
CC INHIBITED BY THE DIURETIC AMILORIDE. MEDIATE THE ELECTRODIFFUSION
CC OF THE LUMINAL SODIUM (AND WATER, WHICH FOLLOWS OSMOTICALLY)
CC THROUGH THE APICAL MEMBRANE OF EPITHELIAL CELLS. CONTROLS THE
CC REABSORPTION OF SODIUM IN KIDNEY, COLON, LUNG AND SWEAT GLANDS.
CC ALSO PLAYS A ROLE IN TASTE PERCEPTION.
CC - SUBUNIT: HETEROTRIMER OF TWO ALPHA, ONE BETA AND ONE GAMMA
CC SUBUNIT. A DELTA SUBUNIT CAN REPLACE THE ALPHA SUBUNIT.
CC - SUBCELLULAR LOCATION: Integral membrane protein.
CC - TISSUE SPECIFICITY: EXPRESSED IN KIDNEY, LUNG, AND DISTAL COLON.
CC - LOW EXPRESSION IN LIVER.
CC - SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNELS
CC FAMILY.
CC -----
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CC -----
DR EMBL: AF112185; AAD21244.1; -.
DR GMD: MG1:101782; Scnla.
DR MIM: 602866; -.
DR InterPro: IPR001873; ASC.
DR Pfam: PF00858; ASC; 1.
DR PRINTS: PRO1078; AMINACHANNEL.
DR PROSITE: PS01206; ASC; 1.
KW Ionic channel; Transmembrane; Ion transport; Glycoprotein.
FT DOMAIN 1 110 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 111 131 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 132 589 POTENTIAL.
FT TRANSMEM 590 610 POTENTIAL.
FT DOMAIN 611 698 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 68 71 POLY-GLU.
FT DOMAIN 221 226 POLY-PRO.
FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 424 424 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 538 538 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 445 445 H -> R (IN REF. 2).
FT CONFLICT 555 557 EKE -> YKH (IN REF. 2).
SQ SEQUENCE 699 AA; 78893 MW; 5B083BB8769B017A CRC64;

Query Match 14.7%; Score 420.5; DB 1; Length 699;
Best Local Similarity 23.5%; Pred. No. 3.3e-26;
Matches 152; Conservative 91; Mismatches 231; Indels 173; Gaps 25;

QY 6 GPEEAR-ROPSP-----IVFASNSCMHGLGHVFGPGLSLRRGMAAANV 49

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Db 57 GPEPSPROPTREEEALIEFHRSYRELFOEFCNNTTIGHAIRLVCCKHNMKTAFAVAVL 116
Oy 50 VLSVAFLYQVAREVRYTEFHHQALD--ERESHRLVFPAVTLCTNPLRSL----- 102
Db 117 LCTFGMMYQOAFLEFEY--FSYPSLINTLNSDKLVPAVAVCTLNPRYTKTEIKEDLEE 174
Oy 103 -----TPNDLHMAGSA-----LLGLDPAEHAFLRALGPRPPGPMPS 141
Db 175 LDRITQTLFDLYKYNSTTRQAGRRSTRDLRGALP--HP--LQRLTRPP--PPNPARS 229
Oy 142 -----PTFD-----MAOLY----- 150
Db 230 ARSASSVDNNPQVDRKDKIGFOLCNOBKSCFYQTSVGVDAVREMYRHYINILSR 289
Oy 151 -----ARAGHSIDMLDCRFGRGCPGPNFTITTRM--GKTYTNSGADGELLTTR 203
Db 290 LDPSTPALEEEALSFTECFRNOAPCNOANYSQFHHPYGCNYTENN--KNNSLNMMSSM 348
Oy 204 GGMNGLDIMLDVQOEYLPVWMDNETPEFVGIRVQIHSOEPPITDQLGSGVGYOT 263
Db 349 PGVNNGLSLTRTEQNDFTPL-----LSTVIGARVWAGQDPAFMDGCGFVVRGVE 402
Oy 264 FVSCQOQSLFLPPWGDSSASLNPYEPSPDPLGSPSPSPPYTLMGCRILACTRY 323
Db 403 SISMRKALDSLGNGYGDCT-----ENGSDVPVKNLYPS--KYTQCVCHSCQEN 451
Oy 324 VARKCCGRMYMPGDVPCVSPQOYKNC-----AHPADAILRKDSCA---CPNP 369
Db 452 MIKCCCAIETFP-----KPKGVFECDYLKQSSMGCYCYKLOAAFLSLDLCGFSKCRKP 505
Oy 370 CASTRAKELSMVRIPSRBAARLARKLNSEAYIEN-----VLADIEPEALNYEVEQ 425
Db 506 CSTNTKLSAGSRMPSVKSQDWIFEMLSLONNTYTNKRNGAKLNIFEKELNYTNS 565
Oy 426 KRAVENSELIDIGCGMGLFPGASLTLEILIDYLCEV-----FRDVLGVFWN 474
Db 566 SPSTVWVSLSLNLSQMSLWFGSSVLSVEMALIFDLVITLIMLHRRSR-----YWS 621
Oy 475 ROHSQR-----HSTNLQDEGLGSHRTOVPHLSLGRPPPTPCAVT 515
Db 622 PGKAGARGAREVASTPASSPSPRCPTSPPP--SLPQOGTTPLALT 667

RESULT 6
FANA.HELAS
ID FANA.HELAS STANDARD; PRT; 625 AA.
AC 025011;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE FMRamide-activated amiloride-sensitive sodium channel (FANACH).
OS Helix aspersa (Brown garden snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Helicacea; Helicidae; Helix.
OX NCBI_TaxID=6535;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Nerve;
RX MEDLINE=96107314; PubMed=7501021;
RA Lindegren E., Champigny G., Lazdunski M., Barbry P.;
RT "Cloning of the amiloride-sensitive FMRamide peptide-gated sodium
channel".
RL Nature 378:730-733(1995).
CC -!- FUNCTION: FMRAMIDE-GATED IONOTROPIC RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: MUSCLE AND NERVOUS TISSUE.
CC -!- SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNELS
FAMILY.
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CC -----
CC EMBL: X92113; CAA63084.1; -.
DR InterPro: IPR001873; ASC.
DR Pfam: PF00858; ASC; 1.
DR PROSITE: PS01206; ASC; 1.
KW Ionic channel; Transmembrane; Glycoprotein.
FT DOMAIN 1 67 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 68 89 POTENTIAL.
FT DOMAIN 90 536 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 537 557 POTENTIAL.
FT DOMAIN 558 625 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 578 581 POLY ASN.
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 303 303 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 349 349 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 365 365 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 473 473 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 625 AA; 71350 MW; CF2E7409CA5B82A6 CRC64;

Query Match 14.7%; Score 419; DB 1; Length 625;
Best Local Similarity 22.2%; Pred. No. 3.8e-26;
Matches 136; Conservative 99; Mismatches 191; Indels 186; Gaps 20;

Oy 17 IRFVAFNSNMGHGIVHPGSLSLRGMMAAVLVSAVFLYQVAREVRYTEFHHQAL 76
Db 43 IABLGSESNHGLAKTYTSD--TKRKYVALLVYAGTATLQSLVKRYLOFOVELS 101
Oy 77 DERESHRLVFPAVTLCONINP-----LRR--SRTPNDLHMAGSALLGLDPAEHAFLRA 128
Db 102 EIKDSMPVOYPSVINCINIEPISLRTIRMYFNESONLITWL--RFLOKRFQDSEFMS 159
Oy 129 LGRPPAPRGMPPTF--DMAQLYARAGSLDMLDCRRGRCGCPGPNFTTFT--RMCK 185
Db 160 I-----RAFYENGDAKKLSHNLMLKRNRLCHVSNSTFDCGNYFN 207
Oy 186 CYTFNSGADGAEILTTTRGGMGLDMLDVQOEYLP-----VWRDNEETPFVGVIRVOI 241
Db 208 CFTFNSG-----QRLQMHATGPENGSLTFSEKDDPLPGYGYVYNDNNTLHSAGRVYV 263
Oy 242 HSQEEPTIIDQLGVSPGYQTFVSCQOQSLFLPPWGDSSASLN--PNYEPSPDPL 299
Db 264 HAPGSMPSPYDHGIDIPPGYSSVGLKAILHTRLPYPYGCNTDMLNGIKQYK----- 316
Oy 300 GSPSPSPSPPYTLMGCRILACTETRYVARKCGCRMYVMPGDV----- 340
Db 317 -----YTFPACLDQKRLIIRCGCKSSALP--EVPYNATFCGYIKDQEIERN 365
Oy 341 -----VCSPOQYKNCARPAIDAILRKD-----SCACPNPCASTR 374
Db 366 HSNMHDHNSQEDRAFIPTPLACBERQKN-----LNDRTYELSCGCGPCQSETS 416
Oy 375 YAKELSMVRIP-----SRAARFLARKLNRESEAVIA----- 405
Db 417 YLKSVSLSYPLFEGYQLSAVERFKQERQAGNHFMKTAVEYLEKLAHPQKHLARDSH 476
Oy 406 -----ENVLADLFEFALNTEYBQKAYKMSLLDDIGG 440
Db 477 MDDLKSYSLSEKAKASDLIRQMLNLNTLYEDLSVEYRQLPAVGLADLFADIGG 536
Oy 441 QMGLFASLTLTLEILDYCEVFRDKVLGVFPNNRQ-----HSQRHS 482
Db 537 TLGLMGISVLTIMLEILYI-----RLTGLVENSEGLPRGTYVNNNNGSNHSG--ST 590
Oy 483 STNLDGLGSH 494
Db 591 SQHQLYNGYMDH 602

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RESULT 7
SCB2_XENLA          STANDARD:      PRT:      646 AA.
ID  SCB2_XENLA
AC  013262:
DT  15-JUL-1998 (Rel. 36, Created)
DT  15-JUL-1998 (Rel. 36, Last sequence update)
DT  15-JUL-1998 (Rel. 36, Last annotation update)
DE  Amiloride-sensitive sodium channel beta-2 subunit (Epithelial Na(+)
DE  channel beta-2 subunit) (Beta-2 ENAC) (Nonvoltage-gated sodium channel
DE  1 beta-2 subunit) (SCNBE2) (Beta-2 NACH).
OS  Xenopus laevis (African clawed frog).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC  Xenopodinae; Xenopus.
OX  NCBI_TaxID=8355;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Puoti A., May A., Rosslar B.C., Horisberger J.D.;
RL  Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC  FUNCTION: SODIUM PERMEABLE NON-VOLTAGE-SENSITIVE ION CHANNEL
CC  INHIBITED BY THE DIURETIC AMILORIDE. MEDATE THE ELECTRODIFFUSION
CC  OF THE LUMINAL SODIUM (AND WATER, WHICH FOLLOWS OSMOTICALLY)
CC  THROUGH THE APICAL MEMBRANE OF EPITHELIAL CELLS. CONTROLS THE
CC  REABSORPTION OF SODIUM IN KIDNEY, COLON, LUNG AND SWEAT GLANDS.
CC  ALSO PLAYS A ROLE IN TASTE PERCEPTION.
CC  -1- SUBUNIT: HETEROTRIMER OF AN ALPHA, BETA AND GAMMA SUBUNIT, A DELTA
CC  SUBUNIT CAN REPLACE THE ALPHA SUBUNIT.
CC  -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC  -1- SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNELS
CC  FAMILY.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: Y12000; CAA72729.1; -.
DR  InterPro: IPR001873; ASC.
DR  Pfam: PF00858; ASC.1.
DR  PRINTS: PRO1078; AMINACHANNEL.
DR  KIR: PROSITE; PS01206; ASC.1.
KW  Ionic channel; Transmembrane; Ion transport; Glycoprotein.
FT  DOMAIN 1 56 CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM 57 77 POTENTIAL.
FT  DOMAIN 78 552 EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM 553 572 POTENTIAL.
FT  DOMAIN 573 646 CYTOPLASMIC (POTENTIAL).
FT  CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 217 217 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 278 278 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 383 383 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 429 429 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 468 468 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ  SEQUENCE 646 AA: 74112 MW: 30126C9D864BFBF0 CRC64;

Query Match 14.68; Score 417; DB 1; Length 646;
Best Local Similarity 22.88; Pred. No. 5.8e-26;
Matches 142; Conservative 93; Mismatches 227; Indels 160; Gaps 23;
QY 20 FASNCSMHGLHVGPGSLRGMMAAVLVATFLYOVAERYRREFHQTALDER 79
DQ 35 FCDMTNHPGRIKES--PKRVMWFLTLVPAGLVFMQGLLITLVSGVSYSL-SI 91
OY 80 ESHRLVPAVTLCLNINPLRSRLTP--NDL-HMAGSAL----- 114
: |||||: ||: ||: ||

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DB 92 GPKTMEFPAVTCNTNPYKYSRKKPLDLDELVATALDRLOYSSOTOANTFTYNNTRON 151
OY 115 LGIDPA--EHAAPFLNALGRPAAPGFMSPFEDMAQLYAR----- 152
DB 152 VTLDPALMNHITLVVIDENDSPN--VIHNIIDNSVFTSKNNMLNNSSEDTGYAQRKV 209
OY 153 -----AGSLDDMLLDCRF 166
DB 210 AMKLCTNNNTQCVYRNFTSGVQALREWYLLQLSIIFSNVPLSDRYDMGRKADLLITLCLE 269
OY 167 KQPCGPEFTTIF--TRMGKCTFNSGADGAEALLTTGGMGNGIDIMLDVQOEYFLVW 225
DB 270 GGQPCSYRNFTHIYADYGNCTIFWVGQEDPTMSNAPGADFLKVLVDLEQDEYLPFL 329
OY 226 RDNEEFPEVGIKVOIHSEEPPIIDGLGVSPCYQFVSCQOOQLSFLPPMGDC--- 282
DB 330 QTT-----AAARLLHQRSFPFYKDLGYAKPETERISIANLVQLOOMEAPYSCTVYN 383
OY 283 -SSASINPYEPEPSDPLGSPSPSPPTLMGCRACETRYVARKGCR--MYMPGDV 339
DB 384 GSDIPVQNLVEEFNS-----YSIQSCLRSCYQEEWVKCKAHYOYPLPNGS 431
OY 340 PYCSPQOYKN---CAHPAIDALTRKDS--ACPNCASSTRAKELSMYRISRAARLA 394
DB 432 EYCTNNKHPDWPCYGLRDSVAIRENCTSLCQCPNDTHKMWISMDWPSAGAEWDIF 491
OY 395 RKLN--RESEAY-IAEN---VLALDIFFEALNYEYQKAVEMSELGDIGOMGLFTGA 448
DB 492 HLYSEKXSDYDTVNRNGIIRLNITYPEFENRISSEBAFVWVLLNLGQFQFMWNG 551
OY 449 SLTLLEILDYCE---VPRDKVLGYFNW-ROHSOR-----HSTNL-LQE 489
DB 552 SVLCIEEGEIIIDMWITIKLWIMINRRORROPYADPPPYSELVBAHTNPGQH 611
OY 490 GIGSHRTQVPHSLGRPPPTP 511
DB 612 DDGNHYTE-----DIPGTPP 626

RESULT 8
SCAB_XENLA
ID  SCAB_XENLA          STANDARD:      PRT:      647 AA.
AC  P51169:
DT  01-OCT-1996 (Rel. 34, Created)
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Amiloride-sensitive sodium channel beta-subunit (Epithelial Na+
DE  channel beta subunit) (Beta ENAC) (Nonvoltage-gated sodium channel 1
DE  beta subunit) (SCNEB) (Beta NACH).
OS  Xenopus laevis (African clawed frog).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC  Xenopodinae; Xenopus.
OX  NCBI_TaxID=8355;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Puoti A., May A., Canessa C.M., Horisberger J.D., Schild L.,
RA  Rosslar B.C.;
RL  MEDLINE=9538264; PubMed=7631745;
RL  Am. J. Physiol. 269:C188-C197(1995).
RT  "The highly selective low-conductance epithelial Na channel of
RT  Xenopus laevis A6 kidney cells."
CC  FUNCTION: SODIUM PERMEABLE NON-VOLTAGE-SENSITIVE ION CHANNEL
CC  INHIBITED BY THE DIURETIC AMILORIDE. MEDATE THE ELECTRODIFFUSION
CC  OF THE LUMINAL SODIUM (AND WATER, WHICH FOLLOWS OSMOTICALLY)
CC  THROUGH THE APICAL MEMBRANE OF EPITHELIAL CELLS. CONTROLS THE
CC  REABSORPTION OF SODIUM IN KIDNEY, COLON, LUNG AND SWEAT GLANDS.
CC  ALSO PLAYS A ROLE IN TASTE PERCEPTION.
CC  -1- SUBUNIT: HETEROTRIMER OF TWO ALPHA, ONE BETA AND ONE GAMMA
CC  SUBUNIT. A DELTA SUBUNIT CAN REPLACE THE ALPHA SUBUNIT (BY
CC  SIMILARITY).
CC  -1- SUBCELLULAR LOCATION: Integral membrane protein.

```

CC -1- SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNELS
 CC FAMILY.
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 DR EMBL: U05285; AAA74971.1; -.
 DR InterPro: IPR001873; ASC.
 DR Pfam: PF00858; ASC; 1.
 DR PRINTS: PRO1078; AMINCHANNEL.
 DR PROSITE: PS01206; ASC; 1.
 KM Ionic channel; Transmembrane; Ion transport; Glycoprotein.
 FT DOMAIN 1
 FT TRANSMEM 57 77
 FT DOMAIN 78 553
 FT TRANSMEM 554 573
 FT DOMAIN 574 647
 FT CARBOHYD 147 147
 FT CARBOHYD 152 152
 FT CARBOHYD 191 191
 FT CARBOHYD 196 196
 FT CARBOHYD 218 218
 FT CARBOHYD 226 226
 FT CARBOHYD 279 279
 FT CARBOHYD 384 384
 FT CARBOHYD 398 398
 FT CARBOHYD 430 430
 FT CARBOHYD 469 469
 FT CARBOHYD 504 504
 SQ SEQUENCE 647 AA; 73976 MW; 3A85366BF0F316 CRC64;
 Query Match 14.6%; Score 415.5; DB 1; Length 647;
 Best Local Similarity 22.0%; Pred. No. 7.6e-26;
 Matches 135; Conservative 92; Mismatches 231; Indels 155; Gaps 19;

DB 493 HVLSKEDSSNITVNRNGRIYLVITFOERNYSISESTNTWVLSNLGGGPFWMGG 552
 QY 449 SLATILELIDLYCEFRDKYGYF-WNRQHSORHSSTNLLQEGLSHRTQVPHLSGPRP 507
 DB 553 VSLCIIIEFGELIIDCMWITLTKFLAMSRNNRRKKR-----PQY 591
 QY 508 PTPPCATYTKLISA 520
 DB 592 SDPEPTVSELVEA 604
 RESULT 9
 SCAA_RAT STANDARD; PRT; 698 AA.
 ID SC37089; Q64593;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Amiloride-sensitive sodium channel alpha-subunit (Epithelial Na+
 DE channel alpha subunit) (Alpha ENaC) (Nonvoltage-gated sodium channel
 DE 1 alpha subunit) (SCN5A) (Alpha NaCh).
 GN SCN5A OR RENAC.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ON NCBI_TaxID=10116;
 RX STRAIN=MSTAR; TISSUE=Distal colon;
 RX MEDLINE=93170495; PubMed=8382172;
 RA Lingueglia E., Volley N., Waldmann R., Lazdunski M., Barbry P.;
 RT "Expression cloning of an epithelial amiloride-sensitive Na+ channel.
 RT A new channel type with homologues to Caenorhabditis elegans
 RT degenerins.";
 RT FEBS Lett. 318:95-99(1993).
 RN [12]
 RP SMOUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Colon epithelium;
 RX MEDLINE=93156815; PubMed=8381523;
 RA Canessa C.M., Horisberger J.D., Rossier B.C.;
 RT "Epithelial sodium channel related to proteins involved in
 RT neurodegeneration.";
 RL Nature 361:467-470(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mistar Kyoto, AND SHRSF; TISSUE=Kidney;
 RX MEDLINE=97191134; PubMed=9039092;
 RA Kreutz R., Strub B., Rubattu S., Hubner N., Szpirer J., Szpirer C.,
 RA Ganten D., Lindpaintner K.;
 RT "Role of the alpha-, beta-, and gamma-subunits of epithelial sodium
 RT channel in a model of polygenic hypertension.";
 RL Hypertension 29:131-136(1997).
 RN [4]
 RP TOPOLOGY, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=95014183; PubMed=7929098;
 RA Snyder P.M., McDonald F.J., Stokes J.B., Welsh M.J.;
 RT "Membrane topology of the amiloride-sensitive epithelial sodium
 RT channel.";
 RL J. Biol. Chem. 269:24379-24383(1994).
 RN [5]
 RP TOPOLOGY.
 RX MEDLINE=94230383; PubMed=8175716;
 RA Renard S., Lingueglia E., Volley N., Lazdunski M., Barbry P.;
 RT "Biochemical analysis of the membrane topology of the amiloride-
 RT sensitive Na+ channel.";
 RL J. Biol. Chem. 269:12981-12986(1994).
 RN [6]
 RP MUTAGENESIS OF SER-589 AND SER-593.
 RX MEDLINE=95263507; PubMed=7744818;
 RA Waldmann R., Champigny G., Lazdunski M.;
 RT "Functional degenerate-in-containing chimeras identify residues essential
 RT for amiloride-sensitive Na+ channel function.";

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RL J. Biol. Chem. 270:11735-11737(1995).
CC - FUNCTION: SODIUM PERMEABLE NON-VOLTAGE-SENSITIVE ION CHANNEL.
CC INHIBITED BY THE DIURETIC AMILORIDE. MEDIANE THE ELECTRODIFFUSION
CC OF THE LUMINAL SODIUM (AND WATER, WHICH FOLLOWS OSMOTICALLY)
CC THROUGH THE APICAL MEMBRANE OF EPITHELIAL CELLS. CONTROLS THE
CC REABSORPTION OF SODIUM IN KIDNEY, COLON, LUNG AND SWEAT GLANDS.
CC ALSO PLAYS A ROLE IN TASTE PERCEPTION.
CC - SUBUNIT: HETEROPTRAMER OF TWO ALPHA, ONE BETA AND ONE GAMMA
CC SUBUNIT. A DELTA SUBUNIT CAN REPLACE THE ALPHA SUBUNIT.
CC - SUBCELLULAR LOCATION: Integral membrane protein.
CC - SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNELS
CC FAMILY.
CC -----
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CC -----
DR EMBL: X70521; CAA49916.1; ALT_INIT.
DR EMBL: X70457; CAA49905.1; -.
DR EMBL: U54699; AAB61156.1; -.
DR EMBL: U54700; AAB61157.1; -.
DR PIR: S29499; S29499.
DR InterPro: IPR001873; ASC.
DR Pfam: PRO0858; ASC. 1.
DR PRINTS: PRO1078; AMINCHANNEL.
DR PROSITE: PS01206; ASC. 1.
KW Ionic channel; Transmembrane; Ion transport; Glycoprotein.
FT DOMAIN 1 110 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 132 131 POTENTIAL.
FT TRANSMEM 590 589 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 611 630 POTENTIAL.
FT CARBOHYD 190 190 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 259 259 N-LINKED (GLCNAc. . .).
FT CARBOHYD 320 320 N-LINKED (GLCNAc. . .).
FT CARBOHYD 339 339 N-LINKED (GLCNAc. . .).
FT CARBOHYD 424 424 N-LINKED (GLCNAc. . .).
FT CARBOHYD 538 538 N-LINKED (GLCNAc. . .).
FT MUTAGEN 588 588 S->I: CHANGES FUNCTION OF THE CHANNEL
INCLUDING CONDUCTANCE, GATING,
SELECTIVITY AND VOLTAGE DEPENDENCE.
FT MUTAGEN 592 592 S->T: CHANGES FUNCTION OF THE CHANNEL
INCLUDING CONDUCTANCE, GATING,
SELECTIVITY AND VOLTAGE DEPENDENCE.
FT CONFLICT 598 599 EL -> DV (IN REF. 2).
FT SEQUENCE 698 AA; 78887 MW; BOCF7C15C3CE9763 CRC64;
SQ
Query Match 14.5%; Score 414.5; DB 1; Length 698;
Best Local Similarity 22.9%; Pred. No. 1e-25;
Matches 147; Conservative 97; Mismatches 236; Indels 161; Gaps 21;
QY 6 GPE-EAROPSD-----IRVFASNCNMHGLGVFGGSLSRGMAAAV 49
DB 57 GPEPSAPROPTDEEALIEFHSRYRELFOFCNNNTIHGAILRVCSEHNMKAFWA--- 113
QY 50 VLSVAFFLVOAERVRKYREF-HHQTALD-ERSHRLVPAVAVLCINPLRARRL----- 102
DB 114 VLMWCFGMKMYQFALLFEFEYLSYPVSLNTLNMSDKLVFPAVYVCTLNPRYREIEELE 173
QY 103 -----FPNDLHMWAGSALLGDPAEHNAFALGAPRAPGPFMDPTDMAQLVARAG 154
DB 174 ELDRTEQTLDFLDYKNSSITRQAGARRSSRLDCAFPRLDRLRTPPPYSGRTARRSG 233
QY 155 HS----- 156
DB 234 SSSVYRONNPVDRKDKIGFQLCNQKSDCFYQTYSQGVDAVREMYRFHYINITLSRLSDT 293
QY 157 -----LDDMLDCRFRCQPCGPENFTTIFTRM-GKCTYPSGADGAEALLTTTGGMG 207

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DB 294 SPALBEALGNFIETCFRNOAPCNOANSKREHPMYGNCYTFND-KNNSNLMSMSPGVN 352
QY 208 NGLDMLDVQOEYLPVRWDRNEPEFVGIRYQHSOEPPLIDGLGVSPGYQTEVSC 267
DB 353 NGLSLTLRTEQDIFPL-----LSTVGARVMYHGDEPAFMDGGNLRPGVETISIM 406
QY 268 QOOQLSFPPPGSSASLANPNEPSPDLPSPSPSPPTLMLGRCLACETRYVARK 327
DB 407 RKEALDSLGNVGDCT-----ENGSDVPYKNLYPS---KYTQOVCIHSCFOENMIKK 455
QY 328 CCCRWY--MPEDVYVCSPOQ-----YKNCAPALDAILRKDSC--ACDPCASIRY 375
DB 456 CCCAVTFPPKPGVEFCYRKQSSWGYCYKLGAFSLDSL---GCFSKCRKPCSVINY 511
QY 376 AKELSNVRIPSRRAARFLARKLNREAYIAEN---VLALDIFEPALNYETVEOKAYEM 431
DB 512 KLSAGYKRPYSKSDQWIFEMSLONNTINKRNGVAKLNFEFLMYKYNSESPVTM 571
QY 432 SELLDIGQWGLTGASLTLEILDYLCY-----FDDKVLGYFWNRQHSOR 480
DB 572 VALLSNLGSQMSLWFGSSVLYVEMAEILFDLVTLLMLLRFRSR---YWSPRGAR 627
QY 481 -----HSTNLLQGLSGHRTQVPHLSLGPAPPPTCAVT 515
DB 628 GAREVASTPASSPSPSRCPHTSPPP-SLPQGGMTPLALT 667

RESULT 10
SCAA_HUMAN STANDARD; PRT; 669 AA.
ID SCAA_HUMAN
AC P37088;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Amiloride-sensitive sodium channel alpha-subunit (Epithelial Na+
DE channel alpha subunit) (SCN5A) (Alpha NaCh).
DE 1 alpha subunit (SCN5A) (Alpha NaCh).
GN SCNN1A OR SCNN1I.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN 11
RN SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=94105144; PubMed=8278374;
RA Volley N., Languegla E., Champigny G., Mattei M.-G., Waldmann R.,
RA Lazdunski M., Barbry P.;
RT "The lung amiloride-sensitive Na+ channel: biophysical properties,
RT pharmacology, ontogenesis, and molecular cloning.";
RT Proc. Natl. Acad. Sci. U.S.A. 91:247-251(1994).
RN 12
RN SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=94295729; PubMed=8023962;
RA McDonald F.J., Snyder P.M., McCray P.B., Welsh M.J.;
RT "Cloning, expression, and tissue distribution of a human amiloride-
RT sensitive Na+ channel.";
RL Am. J. Physiol. 266:L728-L734(1994).
RN 13
RN SEQUENCE FROM N.A.
RX MEDLINE=98316780; PubMed=9654208;
RA Ludwig M., Boikenius U., Wickett L., Marynen P., Bldingmaier F.;
RT "Structural organisation of the gene encoding the alpha subunit of
RT the human amiloride-sensitive epithelial sodium channel.";
RL Hum. Genet. 102:576-581(1998).
RN 14
RN SEQUENCE FROM N.A.
RX MEDLINE=99374783; PubMed=10447117;
RA Chow Y.H., Wang Y., Plumb J., O'Brodoovich H., Hu J.;
RT "Hormonal regulation and genomic organization of the human amiloride-
RT sensitive epithelial sodium channel alpha subunit gene.";
RL Pediatr. Res. 46:208-214(1999).

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CC -1- FUNCTION: SODIUM PERMEABLE NON-VOLTAGE-SENSITIVE ION CHANNEL.
CC INHIBITED BY THE DIURETIC AMILORIDE. MEDIATE THE ELECTRODIFFUSION
CC OF THE LUMINAL SODIUM (AND WATER, WHICH FOLLOWS OSMOTICALLY)
CC THROUGH THE APICAL MEMBRANE OF EPITHELIAL CELLS. CONTROLS THE
CC REABSORPTION OF SODIUM IN KIDNEY, COLON, LUNG AND SWEAT GLANDS.
CC ALSO PLAYS A ROLE IN TASTE PERCEPTION.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA, ONE BETA AND ONE GAMMA
CC SUBUNIT. A DELTA SUBUNIT CAN REPLACE THE ALPHA SUBUNIT.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- DISEASE: DEFECTS IN SCNNIA ARE ONE OF THE CAUSES OF
CC PSEUDOHYPONATREMIA TYPE 1 (PHA1), A RARE SALT WASTING DISEASE
CC CHARACTERIZED BY AN OFTEN FULMINANT PRESENTATION IN THE NEONATAL
CC PERIOD WITH DEHYDRATION, HYPONATREMIA, HYPERKALAEMIA, METABOLIC
CC ACIDOSIS, FAILURE TO THRIVE AND WEIGHT LOSS.
CC -1- SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNELS
CC FAMILY.
CC -----
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DR EMBL: X76180; CAA53773.1; -
DR EMBL: I29007; AAA21813.1; -
DR EMBL: Z82978; CAB07505.1; -
DR EMBL: Z82979; CAB07505.1; JOINED.
DR EMBL: Z82980; CAB07505.1; JOINED.
DR EMBL: Z82981; CAB07505.1; JOINED.
DR EMBL: AF060913; AAD28355.1; -
DR EMBL: AF060910; AAD28355.1; JOINED.
DR EMBL: AF060911; AAD28355.1; JOINED.
DR EMBL: AF060912; AAD28355.1; JOINED.
DR MIM: 600228; -
DR MIM: 177735; -
DR MIM: 264350; -
DR InterPro: IPR001873; ASC.
DR Pfam: PF00858; ASC.1
DR PRINTS: PR01078; AMINCHANNEL.
DR PROSITE: PS01206; ASC.1.
KW Ionic channel; Transmembrane; Ion transport; Glycoprotein.
FT DOMAIN 1 85 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 86 106 POTENTIAL.
FT DOMAIN 107 562 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 563 583 POTENTIAL.
FT DOMAIN 584 669 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 312 312 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 511 511 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 669 AA; 75703 MW; 2CCF342E7DF32E72 CRC64;

Query Match 14.3%; Score 407.5; DB 1; Length 669;
Best local similarity 22.2%; Pred. No. 3.5e-25;
Matches 152; Conservative 96; Mismatches 225; Indels 211; Gaps 26;

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DB 201 RRAASVASSLRDNNPQYDMKWKIGFOLCQNKSDCFYOTSSGVDVAREMYRPHYNIL 260
QY 154 -----GHSDDMLDRCFRGPGCPENFTITFTSM-GKCTYFNGAGACELTT 201
DB 261 SRLEPTELPSLEETLIGFIFACRNOVSCQANYSRHHADYNCYTFND-KNNNSLMS 319
QY 202 TRGGMGGLDMLDVOOEFLPVWRONEETPFEVIGIRVOHSOEEPIIDOLGIVSGY 261
DB 320 SMGICNGSLMLRAEDNDITPL-----ISTYGARVNVHGDPEAFMDGDFNLPGV 373
QY 262 QTEVSCQOQLSPFPWGDSSASLNPNEYEPSPD-PLGSPSPSPPTLMGCRACE 320
DB 374 ETSISMKEKELDLRGDYGQOTK-----NCSDPVENLVPSS---KTYOVCISHC 421
QY 321 TRYVAKRCGRMYMPGDVYVCSPOQYKNCANPAIDAILKDS----- 363
DB 422 QESMKKEGCAIYIFP-----RPONEYCDY-----RKHSWGVCYKLOVDFSSDH 468
QY 364 -----CACPNPCASTRYAKELSMVRIIPRAAARFLARKLNSEAYIAEN-----VLALDIF 415
DB 469 LGCTTKRKRCPCSTYSLGAGYSRHPSVTSEWYFOMLSHONNTYVNNKRYAKVITF 528
QY 416 EALNVEYEQKRAYEMSELLDGGOMLFTGASLTILTEILDYCEV-----F 464
DB 529 KELNYKTNSESPSVYTVTLTSLNCSQMSLMFGSSVLSVEMAEVFDLIVIMLLRLRF 588
QY 465 RDKVLGTFYNNRQHSQRHS--TNLDGELGSHRQVH--LSIGPPPPPPCAVTK--- 516
DB 589 RSR---YWSPPGRGRGAQEVASTLASSPPSH-FCBPHMPSLSLOPPAPSPALTAAPP 642
QY 517 -----TLASHRQCYL 527
DB 643 AYATLGRPPSPGSGAGASSSTCPL 666

RESULT 11
SCAA_BOVIN
ID SCAA_BOVIN STANDARD; PRT; 650 AA.
AC P55270; O02851.
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-OCT-2001 (Rel. 40, Last annotation update)
DE Amiloride-sensitive sodium channel alpha-subunit (Epithelial Na+
DE channel alpha subunit) (Alpha ENaC) (Nonvoltage-gated sodium channel
DE 1 alpha subunit) (SCNNA) (Alpha NaCh).
GN SCNNA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=96032429; Pubmed=7573394;
RA Fuller C.M., Awayda M.S., Arrate M.P., Bradford A.L., Morris R.G.,
RA Ganesa C.M., Rossier B.C., Benos D.J.,
RT "Cloning of a bovine renal epithelial Na+ channel subunit.";
RL Am. J. Physiol. 269:C641-C654(1995).
RN [2]
RP REVISIONS TO C-TERMINUS.
RA Benos D.J.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: SODIUM PERMEABLE NON-VOLTAGE-SENSITIVE ION CHANNEL
CC INHIBITED BY THE DIURETIC AMILORIDE. MEDIATE THE ELECTRODIFFUSION
CC OF THE LUMINAL SODIUM (AND WATER, WHICH FOLLOWS OSMOTICALLY)
CC THROUGH THE APICAL MEMBRANE OF EPITHELIAL CELLS. CONTROLS THE
CC REABSORPTION OF SODIUM IN KIDNEY, COLON, LUNG AND SWEAT GLANDS.
CC ALSO PLAYS A ROLE IN TASTE PERCEPTION.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA, ONE BETA AND ONE GAMMA
CC SUBUNIT. A DELTA SUBUNIT CAN REPLACE THE ALPHA SUBUNIT.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNELS

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U14944; AAB48988.1; -.
CC InterPro: IPR001873; ASC.
CC Pfam: PF00858; ASC.
CC PRINTS: PRO1078; AMINACHANNEL.
CC PROSITE: PS01206; ASC.
CC Ionic channel; Transmembrane; Ion transport; Glycoprotein.
CC DOMAIN 1 65 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 66 86 POTENTIAL.
CC DOMAIN 87 543 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 544 564 POTENTIAL.
CC DOMAIN 565 650 CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 212 212 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 378 378 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 492 492 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 650 AA; 73793 MW; C17CB6C1ECB60B9A CnC64;
CC -----
Query Match 14.0%; Score 400; DB 1; Length 650;
Best Local Similarity 21.8%; Pred. No. 1.4e-24;
Matches 145; Conservative 96; Mismatches 226; Indels 198; Gaps 25;

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OY 471 YFNRHOSHSSTNLDGLCSHRTQ-----VPHLS-LGPRPTPCAVT 515
DB 573 -YWS-----PGRGKGTOEVASTRPASLSPSCFPHAFSSPPDP--A1S 615
OY 516 KTLA 520
DB 616 PALSA 620

RESULT 12
SCAG_RAT STANDARD: PRT: 650 AA.
AC P37091.
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Amloride-sensitive sodium channel gamma-subunit (Epithelial Na+
DE channel gamma subunit) (Gamma ENaC) (Nonvoltage-gated sodium channel
DE 1 gamma subunit) (SCN9G) (gamma NaCh).
GN SCNN9G.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN NM
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-Distal colon epithelium;
RX MEDLINE=94150624; PubMed=8107805;
RA Ganessa C.M., Schild L., Bell G., Thorens B., Gautschi I.,
RA Horişberger J.D., Rossler B.C.;
RA "Amloride-sensitive epithelial Na+ channel is made of three
RT homologous subunits."
RL Nature 367:463-467(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-WISTAR; TISSUE-Distal colon;
RX MEDLINE=94245676; PubMed=8188647;
RA Linguella R., Renard S., Waldmann R., Volley N., Champigny G.,
RA Plass H., Lazdunski M., Barbry P.;
RT "different homologous subunits of the amloride-sensitive Na+ channel
RT are differently regulated by aldosterone."
RL J. Biol. Chem. 269:13736-13739(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-Distal colon, and kidney;
RX MEDLINE=97191134; PubMed=9039092;
RA Kreutz R., Struk B., Rubattu S., Hubner N., Szpirer J.,
RA Szpirer C., Ganten D., Lindpaintner K.;
RT "Role of the alpha-, beta-, and gamma-subunits of epithelial sodium
RT channel in a model of polygenic hypertension."
RL Hypertension 29:131-136(1997).
CC -1- FUNCTION: SODIUM PERMEABLE NON-VOLTAGE-SENSITIVE ION CHANNEL
CC INHIBITED BY THE DIURETIC AMLODIDE. MEDIATE THE ELECTRODIFFUSION
CC OF THE LUMINAL SODIUM (AND WATER, WHICH FOLLOWS OSMOTICALLY)
CC THROUGH THE APICAL MEMBRANE OF EPITHELIAL CELLS. CONTROLS THE
CC REABSORPTION OF SODIUM IN KIDNEY, COLON, LONG AND SWEAT GLANDS.
CC ALSO PLAYS A ROLE IN TASTE PERCEPTION.
CC -1- SUBUNIT: HETEROTRIMER OF TWO ALPHA, ONE BETA AND ONE GAMMA
CC SUBUNIT. A DELTA SUBUNIT CAN REPLACE THE ALPHA SUBUNIT.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE AMLODIDE-SENSITIVE SODIUM CHANNELS
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
EMBL: X77933; CAA54905.1; -.
EMBL: X78034; CAA54964.1; -.

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DR EMBL: U37539; AAB58459.1; -.
 DR EMBL: U37540; AAB58460.1; -.
 DR PIR: S41160; S41160.
 DR InterPro: IPR001873; ASC.
 DR Pfam: PF00858; ASC, 1.
 DR PRINTS: PRO1078; AMINACHANNEL.
 DR PROSITE: PS01206; ASC, 1.
 KW Ionic channel; Transmembrane; Ion transport; Glycoprotein.
 FT DOMAIN 1 55 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 56 76 POTENTIAL.
 FT DOMAIN 77 542 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 543 563 POTENTIAL.
 FT DOMAIN 210 210 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 272 272 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 498 498 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT COMFLICT 53 53 R -> P (IN REF. 1).
 FT COMFLICT 573 573 W -> C (IN REF. 1).
 SQ SEQUENCE 650 AA; 74066 MW; 701F9B28B3250D8F CRC64;
 Query Match 14.0%; Score 398.5; DB 1; Length 650;
 Best Local Similarity 23.2%; Pred. No. 1.8e-24;
 Matches 154; Conservative 93; Mismatches 233; Indels 183; Gaps 26;
 Oy 3 PRSGEARRRPSDRIVRASNSMGLGHVFGPGSLRLRGMAAAVYLSVATFLYQVAE 62
 16 PVRGP-QAPTKIDLMHWCMNTNTHGCRRIYVSRG-RLRLIMIAFTLVAALIIWQCL 73
 Oy 63 RRVYRREHHQTALDERESH-RLVFPAYTCINPLRRSR---LTPNDLMWAGSALIG 116
 74 LV-----ESFYVASIVKHQKIDFPATVTCINIPYKYSANSDLLTDLDE-TQALIS 127
 Oy 117 LDPAAHAFLRALGRPA-----PPGF--MPSPTFD-----MAQL-----Y 150
 128 LYGVKESRRRREAGSMPTLEGTPPREFKLPLVFNENEKGRADFGRKRKISGKII 187
 Oy 146 -----MAQL-----Y 150
 188 HKASVNMVHESKLVGFOLCSNDTSDCATYTFSSGINAIOEMYKLIHYNMIAOVAPLEKK 247
 Oy 151 ARAGSHLDMLDRCFRGPGCPENFTITFRM-GKCYTFNSGADGAEITTTTRGMNG 209
 248 IMMSYSAEELVYTCFPGDMSCARNFTELFHHPMYGNCITFNN-KENATITLSTSMGSEFG 306
 Oy 210 LDIMLDVQOEYLPVWRNDETFPEV--GIRVQIHSQEPPIIDOLGVSFGYQTFVS 266
 307 LQVILYINDEY-----NPFLVSTGAKVLIHQNEFYFIEDVGMIEIFAMSTSIG 357
 Oy 267 CQOQDLSPFPWGCSSSLNPNTPEPSPDPLGSPSP--SPPYTLMGRLACETRY 323
 358 MHLTSEFKISEPYSQCTED-----GSDVPNTNINAYSLQICLYSCFQTK 403
 Oy 324 VARKGCGRNMY--MGQDVPVCSPOOYKN---CAHPAIDAILKRD--SCACPNPCASTRY 375
 404 MEKKGCGAQSPPLRPANYCYQHHPNMICYQLYQAFVVEELGCSQVCSQSSFKWM 463
 Oy 376 AKELSMVAPISPAARFLA-----RKLNRESEAYIAENVALDIFEALINYEYV 423
 464 TLTTSLAQPSEASEKWLNLVLTMDQSQINKLKTID-----LAKLLIFKDLNQRST 517
 Oy 424 EOKKAYESELIGDIGOMGLFTIGASLITILEILDYLCBEVPDKVLGYF----- 472
 518 MESPANSTIEMLSNFGDGLMMSCSYVCIEII---EVF--FLDEFSIARROWHKA 570
 Oy 473 ---NRROSHRSSTNITLOEGLSHR---TQVPHLSLGRP-PPTPPCAVTKTISASHT 524
 571 KDMARRROTPTSTETPSSRQGDNDALTDDDLPTFTSAMRLPAPAGSTVPTCPPTPRWT 630
 Oy 525 CYL 527
 Db 631 LRL 633

RESULT 13
 ID SCOA_RABIT STANDARD; PRT; 640 AA.
 AC 097741;
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE Amloride-sensitive sodium channel alpha-subunit (Epithelial Na+ channel alpha subunit) (Alpha ENaC) (Nonvoltage-gated sodium channel 1 alpha subunit) (SCN5A) (Alpha NaCh).
 GN SCN5A.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_Taxid=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kudacke O., Weisz E., Wiener H., Plass H.;
 RT "The rabbit epithelial sodium channel."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: SODIUM PERMEABLE NON-VOLTAGE-SENSITIVE ION CHANNEL INHIBITED BY THE DIURETIC AMiloride. MEDIATES THE ELECTRODIFFUSION OF THE LUMINAL SODIUM (AND WATER, WHICH FOLLOWS OSMOTICALLY) THROUGH THE APICAL MEMBRANE OF EPITHELIAL CELLS. CONTROLS THE REABSORPTION OF SODIUM IN KIDNEY, COLON, LONG AND SWEAT GLANDS. ALSO PLAYS A ROLE IN TASTE PERCEPTION.
 CC -1- SUBUNIT: HETEROETRAMER OF TWO ALPHA, ONE BETA AND ONE GAMMA SUBUNIT. A DELTA SUBUNIT CAN REPLACE THE ALPHA SUBUNIT.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE AMiloride-SENSITIVE SODIUM CHANNELS FAMILY.
 CC -----
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 CC -----
 CC DR EMBL: AJ132108; CA010571.1; -.
 DR InterPro: IPR001873; ASC.
 DR Pfam: PF00858; ASC, 1.
 DR PRINTS: PRO1078; AMINACHANNEL.
 DR PROSITE: PS01206; ASC, 1.
 KW Ionic channel; Transmembrane; Ion transport; Glycoprotein.
 FT DOMAIN 1 65 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 66 86 POTENTIAL.
 FT DOMAIN 87 539 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 540 560 POTENTIAL.
 FT DOMAIN 561 640 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 270 270 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 374 374 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 488 488 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 640 AA; 72734 MW; 17C84C100F69E133 CRC64;
 Query Match 13.7%; Score 392; DB 1; Length 640;
 Best Local Similarity 22.4%; Pred. No. 5.9e-24;
 Matches 146; Conservative 95; Mismatches 252; Indels 158; Gaps 25;
 Oy 6 GPEE-ARRRPSD-----IVFASNSCMHGLGVFGGSLRLRGMAAAV 49
 12 GPEYVAPQPTDEDEALIEFHRSYRELFOFCNNTTTHAIRKYCSKNNRMKTAFAVAVLM 71
 Oy 50 VLSVATFLYQVAERVRYREFHQTALD-ERESHRLVFPAYTCINPLRRSRLTPN--- 105
 72 LCTFGMMYQFG--LLFGYFSYVNLNINMSDKIVFPAYVCTLNPRYREIFETDQKE 129

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OY 106 -----DLHWSALLGLDPAE-----HAFLRALGRPPAPP-----136
OY 130 LDSTIQOTLLDLKRYNSTLEAOPRRHRDVHPLPLQRLRVPPLRLARRANSASSV 189
OY 137 -----GFM-----PSPFDMAQIYAR-----AG 154
OY 190 RDNSPEYGRKDMWIGFOLCQNRSDCFYORSSGVDAVREYRRHYINILSLDSTLSR 249
OY 155 HSLDMLDCRFRCGQPCGPNFTTIFTRM-GKCYTFNSGADGAEALLTTTRGCMGNDIM 213
OY 250 EQLGNFTFCRFNOAFCGDCGNYSHFHHPMYGCYTFND-KNNSSLMSSMPCINNGLSLT 308
OY 214 LDVQOEELVPMWRNEETPEFVGIRVOIHSEEPPIIDQGLGSPGVQTFVSCQOOLS 273
OY 309 LRTEQNDFTPL-----LSTVTGARVWHGODEFAFMDGCFNLRPGVETISIKRKSLD 362
OY 274 FLPPMGDCSSASLNPYEPEPSPDLGSPSPSPS---PPYTLMGCRACETRYARRKCGC 330
OY 363 RLGGDYGDCTQN-----GSDVPVKMLYRSKYQOVCICHSCFQENNVKRCGC 408
OY 331 RMYV--MPGDVPCSPQOYKN---CAHPAIDALIR-KDSC--ACPNPCASTRYAKELSMV 382
OY 409 AYTFYPLPEGEYECDYRKHNSWGYCYKLDFAFSSDRLGCTKCRKPCSVYNELSGAGS 468
OY 383 RIPSRAARFLARKLNSEAYIAEN---VLALDIFFEALNVEVEOKKAAVEMSELGDI 438
OY 469 RWSVTSIDWVFOHLSLQNNYTSNKRNGVAKLNYFRELKYNKNSPSTVWTLSNL 528
OY 439 GCGMGFLGASLTLTLEILDYLEV-----FRDKVLYGFVN-----ROHSORH 481
OY 529 GSGMSLFGSSVLSVEMAEELFDLSYTFLLMLLRFRSR---YWSRGAGAREVAS 584
OY 482 SSTRLLDEGLASHRTQVPHLSLGR-PPV---PPCAVT--KITLSAHRTC 525
OY 585 SPVSLRSPCRPHPTSPSPVQPGPTPLSPAPPAYATLPCLSGSGSAC 635

RESULT 14
SCAG_XENLA STANDARD: PRT: 660 AA.
ID SCAG_XENLA
AC PS1171;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Amloride-sensitive sodium channel gamma-subunit (Epithelial Na+
DE channel gamma subunit) (Gamma ENaC) (Nonvoltage-gated sodium channel
DE 1 gamma subunit) (SCN5G) (Gamma NaCh).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=95358264; Pubmed=7631745;
RA Puoti A., May A., Canessa C.M., Horişberger J.D., Schild L.,
RA Rossler B.C.;
RT The highly selective low-conductance epithelial Na channel of
RT Xenopus laevis A6 kidney cells.
RL Am. J. Physiol. 269:C188-C197(1995).
CC -1- FUNCTION: SODIUM PERMEABLE NON-VOLTAGE-SENSITIVE ION CHANNEL
CC INHIBITED BY THE DIURETIC AMLORIDE. MEDIATE THE ELECTRODIFFUSION
CC OF THE LUMINAL SODIUM (AND WATER, WHICH FOLLOWS OSMOTICALLY)
CC THROUGH THE APICAL MEMBRANE OF EPITHELIAL CELLS. CONTROLS THE
CC REABSORPTION OF SODIUM IN KIDNEY, COLON, LUNG AND SWEAT GLANDS.
CC ALSO PLAYS A ROLE IN TASTE PERCEPTION.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA, ONE BETA AND ONE GAMMA
CC SUBUNIT. A DELTA SUBUNIT CAN REPLACE THE ALPHA SUBUNIT (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE AMLORIDE-SENSITIVE SODIUM CHANNELS

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U25342; AAA7972.1; -.
CC DR InterPro: IPR001873; ASC.
CC DR Pfam: PF00858; ASC. 1.
CC DR PRINTS: PR01078; AMINACHANNEL.
CC DR PROSITE: PS01206; ASC. 1.
CC KW Ionic channel, Transmembrane, Ion transport, Glycoprotein.
CC FT DOMAIN 1 35
CC FT TRANSMEM 56 76 POTENTIAL.
CC FT DOMAIN 77 545 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 546 566 POTENTIAL.
CC FT DOMAIN 567 660 CYTOPLASMIC (POTENTIAL).
CC FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 213 213 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 498 498 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 660 AA; 75622 MW; 67355f6dce50b1c CRC64;

Query Match 13.7%: Score 391.5; DB 1; Length 660;
Best Local Similarity 21.7%: Pred. No. 6;7e-24;
Matches 141; Conservative 105; Mismatches 232; Indels 171; Gaps 23;

OY 3 PTSGPEARQPSDIRFASNCMHGLGH-VFGSGSLRGMMAAVLVSVATFLYOVA 61
OY 17 PVYGP-QAPITYLEMOWYCLNTNTHGCRIVYSG--RLRWITISLTCAVANIFMCA 73
OY 62 ERVRYREFHQALDERESHRLVPAVTLICNINPLRRSL-----TPNDLH 108
OY 74 LLLMSY--YSVASITVTEQKLYPAVTLICNINPLYSVKRMLALEKETSOLENIY 130
OY 109 WAGSALL-----GLDPAHAFLRAL-----129
OY 131 GTEPPLIRSKRDGVNVENSTEDIFLKOPIRLSEYKSGQLVVSVDLTKKRTMSAKVI 190
OY 130 ---GRPPAPGCFM-----PSPTFD-----MAQIYAR--152
OY 191 HRDAESVQDDPENNVMYGFKLDPKNSDCTIFVSSGVNAIQEWMRYLHTNILLAKISMEDKI 250
OY 153 -AGSLDMLDCRFRCGQPCGPNFTTIFTRM-GKCYTFNSGADGAEALLTTTRGCMGNGL 210
OY 251 AMGKADELIYTCFEDGISCDAENFTLFHNPYLCNCTFNS-ARGNILLVSSMGAGLYGL 309
OY 211 DIMLDVQOEELVPMWRNEETPEFVGIRVOIHSEEPPIIDQGLGSPGVQTFVSCQOQ 270
OY 310 KVALYIDEDY-----NPVYSTAAGAKILVHDDDEPFIEYLETETATETIGMQLT 363
OY 271 QLSFLPPMGDCS---SASLNPYEPEPSPDLGSPSPSPSPPYTLMGCRACETRYARR 326
OY 364 ESAKLSDPYSDCTMDGRDVSVENLYNKK-----YTLQICLNSCPREWR 408
OY 327 KCGCRMV--YMPGDVPCSPQOYKN---CAHPAIDALIRK---SCACPNCASTRYAKE 378
OY 409 SCGCAHYDQPLPGKAKYCNVEEYPSWYCYFKVYKOVQOELGQSQSACRESCKEWTLT 468
OY 379 LSWVRIPS-----RAARFLARKLNSEAYIAENVLA-LDIFFEALNVEVEOKKAY 429
OY 469 RSLAKWPSLNSSEMMKRLSWELGEKLKN--LTKNDLANLNFYODLNSRSISEPTY 525
OY 430 EMSLELDIGOMGLFGASLTLTLEI-----LDYLEVEFRDKVLYGFWRNROHSRST 484
OY 526 NIVTLLSFGQLGMWSSCMICVLEIEVFIDSFVVLQWRNRMWENKREKQADETP 585
OY 485 NLDEGLASH-----RQVPHLSLGRPPPP 511

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DB 586 E1PVPMTGHDNPLCVNDICLGEEDPTFNSALQLPOSOSHVPRTPP 634

RESULT 15
SCAG_MOUSE STANDARD: PRT: 655 AA.

ID SCAG_MOUSE PRT: 655 AA.

AC 09W039;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Amloride-sensitive sodium channel gamma subunit (Epithelial Na+ channel gamma subunit) (Gamma Enac) (Nonvoltage-gated sodium channel 1 gamma subunit) (SCN6G) (Gamma NaCh).
SCN6G.
Mus musculus (Mouse).
OOC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
[1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Kidney;
MEDLINE=99345762; PubMed=10409305;
RA Ahn Y.J., Brooker D.R., Kosari F., Harte B.J., Li J., Mackler S.A., Kleyman T.R.;
RT "Cloning and functional expression of the mouse epithelial sodium channel."
RT Am. J. Physiol. 277:F121-F129(1999).
CC - FUNCTION: SODIUM PERMEABLE NON-VOLTAGE-SENSITIVE ION CHANNEL INHIBITED BY THE DIURETIC AMILORIDE. MEDIATES THE ELECTRODIFFUSION OF THE LUMINAL SODIUM (AND WATER, WHICH FOLLOWS OSMOTICALLY) THROUGH THE APICAL MEMBRANE OF EPITHELIAL CELLS. CONTROLS THE REABSORPTION OF SODIUM IN KIDNEY, COLON, LUNG AND SWEAT GLANDS. ALSO PLAYS A ROLE IN TASTE PERCEPTION.
CC - SUBUNIT: HETEROPTRAMER OF TWO ALPHA, ONE BETA AND ONE GAMMA SUBUNIT. A DELTA SUBUNIT CAN REPLACE THE ALPHA SUBUNIT.
CC - SUBCELLULAR LOCATION: Integral membrane protein.
CC - TISSUE SPECIFICITY: LUNG AND KIDNEY.
CC - SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNELS FAMILY.
CC -----
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CC -----
CC EMBL, AF112187; AAD21246.1; -
DR MGD; MG1:104695; Scn19.
DR InterPro: IPR001873; ASC.
DR Pfam: PF00858; ASC; 1.
DR PRINTS: PRO1078; AMINCHANNEL.
DR PROSITE: PS01206; ASC; 1.
KW Ionic channel; Transmembrane; Ion transport; Glycoprotein.
FT DOMAIN 1 55 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 56 76 POTENTIAL.
FT DOMAIN 77 547 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 548 568 POTENTIAL.
FT DOMAIN 569 655 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 215 215 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 254 254 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 503 503 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 655 AA: 74635 MW; ABAADDA9D6160596D CRC64;

Query Match 13.7%; Score 391; DB 1; Length 655;

Best Local Similarity 22.7%; Pred. No. 7 3e-24;

Matches 150; Conservative 90; Mismatches 224; Indels 196; Gaps 25;

3 PTSGPEARROPSPDIRVFASNCMGLGHVFGSLSLRGMAAAVLSVATFLYQVAE 62

DB 16 PVKGP-QAFTIKDLMHWYCLNTNTHGCRITVSRG-RLRRLMIATFLTAVALIINOAL 73

QY 63 RVRYREPHHQTALDERESH--RLVPAVTLGINFLRRSR-----LTPNDLHWAGSALIG 116

DB 74 LV-----FSFYIVSVSIKHFQKLDPRPAYTICININIKYSANSDLLTDLDSE-TRKALLS 127

QY 117 L-----DPAEAAFLRAL--GRPPAPGFMPSPTFD----- 145

DB 128 LVGVKQVLDSTPRKREAGSMRSTWGTPTPRFLNLPVLVFNENKGRADFTGRKRI 187

QY 146 -----MAQL 149

DB 188 SKTIHKASNYMHESKRLVGFQLCSNDTSDCATYTFSSGINAIDEMTKLHYMINIAOV 247

QY 150 ----YRAGSHLDDMLDRCFRGQPCGFENFTIFTRM-GKCYTFNSGAGALLTTTGG 204

DB 248 PLEKTKIMSYSAFELLVYTCFFDGMSCDARNFTLFHPHMGNCITFMN-RENATILSTSMG 306

QY 205 GMNGGLDMLDVOOEYLPVWRDNEETPEV--GIKVOIHSQEPPIIDQLGVSPEG 261

DB 307 GSEYGLQVILYINEDY-----NPLVSTGAKVLVHQNEYPTEIDVGTETETAM 357

QY 262 QTFVSCQOQQLSFLPPWGDSSASLNPVTEPSPDPLGSPSPSP--SPPTLMGCRLA 318

DB 358 STSIGMHLTESFKLSPEYSQCTED-----GSDVPTNINAAVSLQICLYS 403

QY 319 CETRYVARRCGCMYV--MPGDVPCSPQOYKN--CAHPAIDAILRKD--SCAPNPG 370

DB 404 CFOTKWEKCGCAOYSOPLPRAANCYOOHPMMYCYQLOVAFVREELGCOSVCOSK 463

QY 371 ASTRYAKELSMVIPSRAARFLA-----RKINRSEAYIAENVLADIFFEAL 418

DB 464 SPEKWLITSLAMPSEASESKWLLNVLMQSOQINKLTKTD-----LAKLILYKDL 517

QY 419 NRTVDOKAYENSELLGDIGOMGLFICASLTLTIEILDYCEVRDKVLGF----- 472

DB 518 NRSIMESPANSTIEMLSNFGGLGIMSCSVCIIEI---EVF---FIDFFSIARR 570

QY 473 -----NRRHSHSSSTNLLQELG-----SHRTQVPHLSGPRPTPP 511

DB 571 OMOKAKDMMARRRTPPTETPSSQGGQDNPDALDTDDLTPTTSAMRLPAPAEAPVGTTP 630

Search completed: October 11, 2002, 07:24:36

Job time : 41 secs

